

Protein Sequence Searches - February 2005

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- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:38:28 ; Search time 56.732 Seconds
(without alignments)
408.044 Million cell updates/sec

Title: US-10-680-349-42
Perfect score: 1462
Sequence: 1 MNYKKILVRSALISLMSILP.....ASVTLDVGFGEIGMRFTF 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1462	100.0	280	2	US-09-660-587-42 Sequence 42, Appl
2	1462	100.0	280	2	US-09-314-701-48 Sequence 48, Appl
3	1462	100.0	280	2	US-09-811-007A-42 Sequence 42, Appl
4	1462	100.0	280	2	US-10-314-639-48 Sequence 48, Appl
5	1462	100.0	280	2	US-10-059-964A-48 Sequence 48, Appl
6	1202.5	82.3	283	2	US-09-660-587-10 Sequence 10, Appl
7	1202.5	82.3	283	2	US-09-261-358A-10 Sequence 10, Appl
8	1202.5	82.3	283	2	US-09-201-458-6 Sequence 6, Appl
9	1202.5	82.3	283	2	US-09-314-701-4 Sequence 4, Appl
10	1202.5	82.3	283	2	US-09-811-007A-10 Sequence 10, Appl
11	1202.5	82.3	283	2	US-10-314-639-4 Sequence 4, Appl
12	1202.5	82.3	283	2	US-10-059-964A-4 Sequence 4, Appl
13	644.5	44.1	281	2	US-09-660-587-9 Sequence 9, Appl
14	644.5	44.1	281	2	US-09-261-358A-9 Sequence 9, Appl
15	644.5	44.1	281	2	US-09-201-458-5 Sequence 5, Appl
16	644.5	44.1	281	2	US-09-811-007A-9 Sequence 9, Appl
17	642.5	43.9	281	2	US-09-314-701-2 Sequence 2, Appl
18	642.5	43.9	281	2	US-10-314-639-2 Sequence 2, Appl
19	642.5	43.9	281	2	US-10-059-964A-2 Sequence 2, Appl
20	642.5	43.9	281	2	US-10-059-964A-67 Sequence 67, Appl
21	629.5	43.1	276	2	US-08-953-326-18 Sequence 18, Appl
22	629.5	43.1	276	2	US-09-553-662-18 Sequence 18, Appl
23	629.5	43.1	276	2	US-10-062-994-18 Sequence 18, Appl
24	621	42.5	288	2	US-09-314-701-32 Sequence 32, Appl
25	621	42.5	288	2	US-10-314-639-32 Sequence 32, Appl
26	621	42.5	288	2	US-10-059-964A-32 Sequence 32, Appl
27	620	42.4	286	2	US-08-953-326-15 Sequence 15, Appl

28	620	42.4	286	2	US-09-660-587-12	Sequence 12, Appl
29	620	42.4	286	2	US-09-261-358A-12	Sequence 12, Appl
30	620	42.4	286	2	US-09-201-458-8	Sequence 8, Appl
31	620	42.4	286	2	US-09-314-701-8	Sequence 8, Appl
32	620	42.4	286	2	US-09-553-662-15	Sequence 15, Appl
33	620	42.4	286	2	US-10-062-994-15	Sequence 15, Appl
34	620	42.4	286	2	US-09-811-007A-12	Sequence 12, Appl
35	620	42.4	286	2	US-10-314-639-8	Sequence 8, Appl
36	620	42.4	286	2	US-10-059-964A-8	Sequence 8, Appl
37	605	41.4	280	2	US-09-660-587-14	Sequence 14, Appl
38	605	41.4	280	2	US-09-261-358A-14	Sequence 14, Appl
39	605	41.4	280	2	US-09-201-458-10	Sequence 10, Appl
40	605	41.4	280	2	US-09-314-701-12	Sequence 12, Appl
41	605	41.4	280	2	US-09-811-007A-14	Sequence 14, Appl
42	605	41.4	280	2	US-10-314-639-12	Sequence 12, Appl
43	605	41.4	280	2	US-10-059-964A-12	Sequence 12, Appl
44	603	41.2	280	2	US-08-953-326-17	Sequence 17, Appl
45	603	41.2	280	2	US-09-553-662-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-660-587-42
; Sequence 42, Application US/09660587
; Patent No. 6392023
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/660,587
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-09-660-587-42

Query Match	100.0%	Score 1462;	DB 2;	Length 280;
Best Local Similarity	100.0%;	Pred. No. 2.1e-151;		
Matches 280;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKEGFYISAKYNPSTSHFRKFSAEET	60	
Db	1	MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKEGFYISAKYNPSTSHFRKFSAEET	60	
QY	61	PINGTNSLTKKVFGGLKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYSGMDGPRIELE	120	
Db	61	PINGTNSLTKKVFGGLKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYSGMDGPRIELE	120	
QY	121	AAQQFNPNTDNDTNGEYKHFALSRKDAEDQYVVLKNDGITFMSLWNTCYDIT	180	
Db	121	AAQQFNPNTDNDTNGEYKHFALSRKDAEDQYVVLKNDGITFMSLWNTCYDIT	180	
QY	181	AEVGSFVPVACAGICADLITIFKDLNLKFPAYGKIGISYPITPEVSATFGGYVHGVGNK	240	
Db	181	AEVGSFVPVACAGICADLITIFKDLNLKFPAYGKIGISYPITPEVSATFGGYVHGVGNK	240	
QY	241	FEKIPVITPVNLNDAPQTTSASVTLDVGFGGEIGMRFTF	280	
Db	241	FEKIPVITPVNLNDAPQTTSASVTLDVGFGGEIGMRFTF	280	

RESULT 2

```
US-09-314-701-48
; Sequence 48, Application US/09314701
; Patent No. 6544517
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohasei, No. 6544517io
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; TITLE OF INVENTION: Chaffensis
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/09/314,701
; CURRENT FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-09-314-701-48

Query Match      100.0%; Score 1462; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.1e-151;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYKKILVRSALISLSILPYQSFADPVGSRRTNDNKEGFYISAKYNPSISHPRKFSABET 60
DB 1 MNYKKILVRSALISLSILPYQSFADPVGSRRTNDNKEGFYISAKYNPSISHPRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYSDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYSDGPRIELE 120
QY 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAEDQQVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAEDQQVVLKNDGITFMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIGADLITIFKDLNLKFAVQKGIGISYPIPTPEVSFAFIGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIGADLITIFKDLNLKFAVQKGIGISYPIPTPEVSFAFIGGYHGVGNK 240
QY 241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEIGMRFTF 280

RESULT 3
US-09-811-007A-42
; Sequence 42, Application US/09811007A
; Patent No. 6660269
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/811,007A
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-09-811-007A-42

Query Match      100.0%; Score 1462; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.1e-151;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYKKILVRSALISLSILPYQSFADPVGSRRTNDNKEGFYISAKYNPSISHPRKFSABET 60
DB 1 MNYKKILVRSALISLSILPYQSFADPVGSRRTNDNKEGFYISAKYNPSISHPRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYSDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYSDGPRIELE 120
QY 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAEDQQVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAEDQQVVLKNDGITFMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIGADLITIFKDLNLKFAVQKGIGISYPIPTPEVSFAFIGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIGADLITIFKDLNLKFAVQKGIGISYPIPTPEVSFAFIGGYHGVGNK 240
QY 241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEIGMRFTF 280

RESULT 4
US-10-314-639-48
; Sequence 48, Application US/10314639
; Patent No. 6893640
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohasei, No. 6893640io
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; TITLE OF INVENTION: Chaffensis
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/10/314,639
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/314,701
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-10-314-639-48

Query Match      100.0%; Score 1462; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.1e-151;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYKKILVRSALISLSILPYQSFADPVGSRRTNDNKEGFYISAKYNPSISHPRKFSABET 60
DB 1 MNYKKILVRSALISLSILPYQSFADPVGSRRTNDNKEGFYISAKYNPSISHPRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYSDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYSDGPRIELE 120
QY 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAEDQQVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAEDQQVVLKNDGITFMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIGADLITIFKDLNLKFAVQKGIGISYPIPTPEVSFAFIGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIGADLITIFKDLNLKFAVQKGIGISYPIPTPEVSFAFIGGYHGVGNK 240
QY 241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEIGMRFTF 280

RESULT 5
US-10-059-964A-48
; Sequence 48, Application US/10059964A
; Patent No. 6923963
; GENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
```


; CURRENT APPLICATION NUMBER: US/10/314,639
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/314,701
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-10-314-639-4

Query Match 82.3%; Score 1202.5; DB 2; Length 283;
Best Local Similarity 79.5%; Pred. No. 5.4e-123;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;
QY 1 MNYKKILVRSALISLSILPYQSFADPVGSR---TNDNKEGFVISAKYNPSISHPRKPSA 57
DB 1 MNYKKILVRSALISLSILPYQSFADPVTSNDTGINDSREGFYISVKYNPSISHPRKPSA 60
QY 58 EETPINGTNSLTKKVFLGKKGDDITKKDDFTRVAPGIDFQNNLISGFSIGYSMDGPRI 117
DB 61 EEAPINGNTSITKKVFLGKKGDDIAQSANFNRTDPALEFQNNLISGFSIGYAMDGPRI 120
QY 118 ELEAAAYQOFPNPKNTDNDTNGEYKHFALSRKDAEDQOYVVLKNDGITFMSLMVNTCY 177
DB 121 ELEAAAYQKFDKPNNDTNSGDIYKYFGLSREDAIADKKYVVLKNEGITFMSLMVNTCY 180
QY 178 DITAEGVSPVPYACAGIGADLITFKDLNLKFAVQKIGISYPIITPEVSAGTGYHGYI 237
DB 181 DITAEGVFPPIYACAGVADLINVDFNLKFSYQKIGISYPIITPEVSAGTGYHGYI 240
QY 238 GNNFKIPVITPVVLNDAPQTTASVTLDVGYFGGEGIGMRFTF 280
DB 241 GNNFNKIPVITPVLEGAQPTTSALVTIDTGYFGGEGVGRFTF 283

RESULT 12
US-10-059-964A-4
; Sequence 4; Application US/10059964A
; Patent No. 6923963
; GENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
; APPLICANT: OHASHI, NORIO
; TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRlichia CANIS AND EHRlichia
; FILE REFERENCE: 22727-04109
; CURRENT APPLICATION NUMBER: US/10/059,964A
; CURRENT FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: 09/314,701
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/100,843
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-10-059-964A-4

Query Match 82.3%; Score 1202.5; DB 2; Length 283;
Best Local Similarity 79.5%; Pred. No. 5.4e-123;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;
QY 1 MNYKKILVRSALISLSILPYQSFADPVGSR---TNDNKEGFVISAKYNPSISHPRKPSA 57
DB 1 MNYKKILVRSALISLSILPYQSFADPVTSNDTGINDSREGFYISVKYNPSISHPRKPSA 60
QY 58 EETPINGTNSLTKKVFLGKKGDDITKKDDFTRVAPGIDFQNNLISGFSIGYSMDGPRI 117
DB 61 EEAPINGNTSITKKVFLGKKGDDIAQSANFNRTDPALEFQNNLISGFSIGYAMDGPRI 120

QY 118 ELEAAAYQOFPNPKNTDNDTNGEYKHFALSRKDAEDQOYVVLKNDGITFMSLMVNTCY 177
DB 121 ELEAAAYQKFDKPNNDTNSGDIYKYFGLSREDAIADKKYVVLKNEGITFMSLMVNTCY 180
QY 178 DITAEGVSPVPYACAGIGADLITFKDLNLKFAVQKIGISYPIITPEVSAGTGYHGYI 237
DB 181 DITAEGVFPPIYACAGVADLINVDFNLKFSYQKIGISYPIITPEVSAGTGYHGYI 240
QY 238 GNNFKIPVITPVVLNDAPQTTASVTLDVGYFGGEGIGMRFTF 280
DB 241 GNNFNKIPVITPVLEGAQPTTSALVTIDTGYFGGEGVGRFTF 283

RESULT 13
US-09-660-587-9
; Sequence 9; Application US/09660587
; Patent No. 6392023
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/660,587
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 9
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis P28
US-09-660-587-9

Query Match 44.1%; Score 644.5; DB 2; Length 281;
Best Local Similarity 48.1%; Pred. No. 6.4e-62;
Matches 140; Conservative 41; Mismatches 89; Indels 21; Gaps 6;
QY 1 MNYKKILVRSALISLSILPYQSFADPVGSRDNDNKEGFYISAKYNPSISHPRKPSABET 60
DB 1 MNYKKVFTTSALISLISLPGVSPDPAGSINGN---FYISGKYMPSASHFGVFSABE- 56
QY 61 PINGTNSLTKKVFLGKKGDD-----ITKKDDFTRVAPGIDFQNNLISGFSIGYSMDG 114
DB 57 -----ERNITTVGVFLGKQNDGSAISNSPNDVTVSNYSFKYENNPFLGFAIGYSMDG 112
QY 115 PRIELEAAAYQOFPNPKNTDNDTNGEYKHFALSRKDAEDQOYVVLKNDGITFMS 170
DB 113 PRIELEVSYETFDVKNQGN--YKNEAHRICALSHNSAADMSASNNFVFLKNEGILLDIS 170
QY 171 LMVNTCYDITAEGVSPVPYACAGIGADLITFKDLNLKFAVQKIGISYPIITPEVSAGT 230
DB 171 FMLNACYDVWGEIGIPFSPYICAGIGTDLVSMPEATNPKISYQKIGLSYSISPEASVFIG 230
QY 231 GYVHGVGNKKEKIPVITPVVLNDAPQ-TTSASVTLDVGYFGGEGIGMRFTF 280
DB 231 GHFHVKVIGNEFRDIPTIITGTLGKGNYPVAILVDVCHFGIELGGRFAP 281

RESULT 14
US-09-261-358A-9
; Sequence 9; Application US/09261358A
; Patent No. 6403780
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP
US-09-261-358A-9

CURRENT APPLICATION NUMBER: US/09/261,358A
CURRENT FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/201,458
PRIOR FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 9
LENGTH: 281
TYPE: PRT
ORGANISM: Ehrlichia chaffeensis
FEATURE:
OTHER INFORMATION: amino acid sequence of E. chaffeensis P28
US-09-261-358A-9

Query Match 44.1%; Score 644.5; DB 2; Length 281;
Best Local Similarity 48.1%; Pred. No. 6.4e-62;
Matches 140; Conservative 41; Mismatches 89; Indels 21; Gaps 6;
QY 1 MNYKILVRSAIISLILPYOSFADPVGSRNDNKEGFIYISAKYNPSISHPRKFSAEET 60
DB 1 MNYKKVFIITSALISLISLPGVSFSDPAGSINGN---FYISGKYMPSASHFGVFSAKE- 56
QY 61 PINGTNSLTQKVFGLKKGD-----ITKDDPTRVAPGIDFQNNLISGFSIGYSMDG 114
DB 57 ----ERNTTVGVLQKQNDGSAISNSPNDVFTVSNYSFKYENNPFLGFAGAIYSMDG 112
QY 115 PRIELEAAVQQFNPKNKTNDNDNGEYKHFALSRKDAME----DQYVVLKNDGITFMS 170
DB 113 PRIELEVSYETFDVKNQGN--YKNEAHRYCALSHNSAADSSASNNFVFLKNEGLLDIS 170
QY 171 LMVNTCYDITAGSVSPVACAGADLITIFKDLNLKPAYQKGIGISYPTPEVSAPIG 230
DB 171 FMLNACYDVVGEGIPSPYICAGIGTDLVSMFEATNPKISYQKGLGYSISPEASVFIG 230
QY 231 GYHGVIGNKFEKIPVITPVVLNDAPQ--TTSASVTLDVGYFGGEGIMRPTF 280
DB 231 GHFHKVIGNFRDPTIITPTGSTLAGKGNYPAILVDVCHFGIELGGRPAF 281

RESULT 15
US-09-201-458-5
Sequence 5, Application US/09201458A
Patent No. 6458942
GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: 28-kDa Immunoreactive Protein Gene of Ehrlichia
TITLE OF INVENTION: canis and Uses Thereof
FILE REFERENCE: D6152
CURRENT APPLICATION NUMBER: US/09/201,458A
CURRENT FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 5
LENGTH: 281
TYPE: PRT
ORGANISM: Ehrlichia chaffeensis
FEATURE:
OTHER INFORMATION: amino acid sequence of E. chaffeensis P28
US-09-201-458-5

Query Match 44.1%; Score 644.5; DB 2; Length 281;
Best Local Similarity 48.1%; Pred. No. 6.4e-62;
Matches 140; Conservative 41; Mismatches 89; Indels 21; Gaps 6;
QY 1 MNYKILVRSAIISLILPYOSFADPVGSRNDNKEGFIYISAKYNPSISHPRKFSAEET 60
DB 1 MNYKKVFIITSALISLISLPGVSFSDPAGSINGN---FYISGKYMPSASHFGVFSAKE- 56
QY 61 PINGTNSLTQKVFGLKKGD-----ITKDDPTRVAPGIDFQNNLISGFSIGYSMDG 114
DB 57 ----ERNTTVGVLQKQNDGSAISNSPNDVFTVSNYSFKYENNPFLGFAGAIYSMDG 112
QY 115 PRIELEAAVQQFNPKNKTNDNDNGEYKHFALSRKDAME----DQYVVLKNDGITFMS 170

DB 113 PRIELEVSYETFDVKNQGN--YKNEAHRYCALSHNSAADSSASNNFVFLKNEGLLDIS 170
QY 171 LMVNTCYDITAGSVSPVACAGADLITIFKDLNLKPAYQKGIGISYPTPEVSAPIG 230
DB 171 FMLNACYDVVGEGIPSPYICAGIGTDLVSMFEATNPKISYQKGLGYSISPEASVFIG 230
QY 231 GYHGVIGNKFEKIPVITPVVLNDAPQ--TTSASVTLDVGYFGGEGIMRPTF 280
DB 231 GHFHKVIGNFRDPTIITPTGSTLAGKGNYPAILVDVCHFGIELGGRPAF 281

Search completed: January 24, 2006, 11:49:00
Job time : 57.732 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:46:59 ; Search time 154.641 Seconds
(without alignments)
756.543 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462

Sequence: 1 MNYKKILVRSALISLSILP.....ASVTLDVGFGEIGMRFTF 280

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

1: /cgn2_5/prodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1462	100.0	280	3	US-09-811-007-42
2	1462	100.0	280	4	US-10-062-624-42
3	1462	100.0	280	4	US-10-059-964-48
4	1462	100.0	280	4	US-10-062-051-42
5	1462	100.0	280	4	US-10-062-920-42
6	1462	100.0	280	4	US-10-314-639-48
7	1462	100.0	280	4	US-10-680-349-42
8	1462	100.0	280	5	US-10-731-554-42
9	1462	100.0	280	5	US-10-901-714-48
10	1462	100.0	280	5	US-10-901-774-48
11	1202.5	82.3	283	3	US-09-846-808-14
12	1202.5	82.3	283	3	US-09-811-007-10
13	1202.5	82.3	283	4	US-10-062-624-10
14	1202.5	82.3	283	4	US-10-059-964-4
15	1202.5	82.3	283	4	US-10-062-051-10
16	1202.5	82.3	283	4	US-10-284-986-14
17	1202.5	82.3	283	4	US-10-062-920-10
18	1202.5	82.3	283	4	US-10-314-639-4
19	1202.5	82.3	283	4	US-10-369-293-14
20	1202.5	82.3	283	4	US-10-285-042-14
21	1202.5	82.3	283	4	US-10-680-349-10
22	1202.5	82.3	283	5	US-10-731-554-10
23	1202.5	82.3	283	5	US-10-901-714-4
24	1202.5	82.3	283	5	US-10-901-774-4
25	644.5	44.1	281	3	US-09-846-808-19
26	644.5	44.1	281	3	US-09-811-007-9
27	644.5	44.1	281	4	US-10-062-624-9

28	644.5	44.1	281	4	US-10-062-051-9	Sequence 9, Appli
29	644.5	44.1	281	4	US-10-284-986-19	Sequence 19, Appli
30	644.5	44.1	281	4	US-10-062-920-9	Sequence 9, Appli
31	644.5	44.1	281	4	US-10-369-293-19	Sequence 19, Appli
32	644.5	44.1	281	4	US-10-285-042-19	Sequence 19, Appli
33	644.5	44.1	281	4	US-10-680-349-9	Sequence 9, Appli
34	644.5	44.1	281	5	US-10-731-554-9	Sequence 9, Appli
35	642.5	43.9	281	4	US-10-059-964-2	Sequence 2, Appli
36	642.5	43.9	281	4	US-10-314-639-2	Sequence 2, Appli
37	642.5	43.9	281	5	US-10-901-714-2	Sequence 2, Appli
38	642.5	43.9	281	5	US-10-901-714-67	Sequence 67, Appli
39	642.5	43.9	281	5	US-10-901-774-2	Sequence 2, Appli
40	642.5	43.9	281	5	US-10-901-774-67	Sequence 67, Appli
41	629.5	43.1	276	4	US-10-062-994-18	Sequence 18, Appli
42	629.5	43.1	276	4	US-10-062-994-18	Sequence 18, Appli
43	629.5	43.1	276	4	US-10-722-077-18	Sequence 18, Appli
44	621	42.5	288	4	US-10-059-964-32	Sequence 32, Appli
45	621	42.5	288	4	US-10-314-639-32	Sequence 32, Appli

ALIGNMENTS

RESULT 1

US-09-811-007-42
; Sequence 42, Application US/09811007
; Publication No. US20030185849A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/811,007
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-09-811-007-42

Query Match	100.0%;	Score 1462;	DB 3;	Length 280;
Best Local Similarity	100.0%;	Pred. No. 9.8e-136;		
Matches 280;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MNYKKILVRSALISLSILPYQSFADPVGSRNDNKEGVYISAKYNPISHPKFSAEET	60	
Db	1	MNYKKILVRSALISLSILPYQSFADPVGSRNDNKEGVYISAKYNPISHPKFSAEET	60	
Qy	61	PINGTNSLTKKVFGKKGDDITFKDDFTFVAPGIDFQNNLISGFSIGSYMDGPRIELE	120	
Db	61	PINGTNSLTKKVFGKKGDDITFKDDFTFVAPGIDFQNNLISGFSIGSYMDGPRIELE	120	
Qy	121	AAQQFNPQNTDNDNGEYVYKHPALSRKDAEDQYVVLKNDGITFMSLMVNTCYDIT	180	
Db	121	AAQQFNPQNTDNDNGEYVYKHPALSRKDAEDQYVVLKNDGITFMSLMVNTCYDIT	180	
Qy	181	AEVGSFVPYACAGICADLITTFKDLNLFAYOGKIGISVPIPEVSATFGGYHGVGNK	240	
Db	181	AEVGSFVPYACAGICADLITTFKDLNLFAYOGKIGISVPIPEVSATFGGYHGVGNK	240	
Qy	241	FEKIPVITPVVLNDAPQTTASVTLDVGFGEIGMRFTF	280	
Db	241	FEKIPVITPVVLNDAPQTTASVTLDVGFGEIGMRFTF	280	

RESULT 2


```
RESULT 5
US-10-062-920-42
; Sequence 42, Application US/10062920
; Publication No. US20030096250A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/10/062,920
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/660,587
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-10-062-920-42

Query Match      100.0%; Score 1462; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 9.8e-136;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGYISAKYNPSISHFRKFSABET 60
DB 1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGYISAKYNPSISHFRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGSYMDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGSYMDGPRIELE 120
QY 121 AAYQFNPKNPTDNDTNGEYKHFALSRKDAMEQQYVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQFNPKNPTDNDTNGEYKHFALSRKDAMEQQYVVLKNDGITFMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIADLITIFKDLNLKFAQKGIGISYPIPEVSFAFIGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIADLITIFKDLNLKFAQKGIGISYPIPEVSFAFIGGYHGVGNK 240
QY 241 FEKIPVITPVNLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVNLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280

RESULT 6
US-10-314-639-48
; Sequence 48, Application US/10314639
; Publication No. US20030103991A1
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohasi, No. US20030103991A10
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/10/314,639
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/314,701
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-10-314-639-48

Query Match      100.0%; Score 1462; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 9.8e-136;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGYISAKYNPSISHFRKFSABET 60
DB 1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGYISAKYNPSISHFRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGSYMDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGSYMDGPRIELE 120
QY 121 AAYQFNPKNPTDNDTNGEYKHFALSRKDAMEQQYVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQFNPKNPTDNDTNGEYKHFALSRKDAMEQQYVVLKNDGITFMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIADLITIFKDLNLKFAQKGIGISYPIPEVSFAFIGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIADLITIFKDLNLKFAQKGIGISYPIPEVSFAFIGGYHGVGNK 240
QY 241 FEKIPVITPVNLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVNLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280

RESULT 7
US-10-680-349-42
; Sequence 42, Application US/10680349
; Publication No. US20040198951A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2/D1
; CURRENT APPLICATION NUMBER: US/10/680,349
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US/10/062,624
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-10-680-349-42

Query Match      100.0%; Score 1462; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 9.8e-136;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGYISAKYNPSISHFRKFSABET 60
DB 1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGYISAKYNPSISHFRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGSYMDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGSYMDGPRIELE 120
QY 121 AAYQFNPKNPTDNDTNGEYKHFALSRKDAMEQQYVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQFNPKNPTDNDTNGEYKHFALSRKDAMEQQYVVLKNDGITFMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIADLITIFKDLNLKFAQKGIGISYPIPEVSFAFIGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIADLITIFKDLNLKFAQKGIGISYPIPEVSFAFIGGYHGVGNK 240
QY 241 FEKIPVITPVNLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVNLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
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Db 241 FEKIPVITPVVNDAPQTTSASVTLDVGVFGGEIGMRFTF 280

RESULT 8

US-10-731-554-42
; Sequence 42, Application US/10731554
; Publication No. US20040247616A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/10/731,554
; CURRENT FILING DATE: 2003-12-09
; PRIOR FILING DATE: US/09/811,007
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-10-731-554-42

Query Match 100.0%; Score 1462; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 9.8e-136;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKEGFYISAKYNPSISHPRKFSABET 60
DB 1 MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKEGFYISAKYNPSISHPRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKDGDITKKDDFTRVAPGIDFQNNLISGFGSGISYMDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKDGDITKKDDFTRVAPGIDFQNNLISGFGSGISYMDGPRIELE 120
QY 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAMEDQQYVVLKNDGITTMSLMVNTCYDIT 180
DB 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAMEDQQYVVLKNDGITTMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIADLITIFKDLNLFKPAYQKGIGISYPITPEVSATFYGYYHGVGNK 240
DB 181 AEGVSFVPYACAGIADLITIFKDLNLFKPAYQKGIGISYPITPEVSATFYGYYHGVGNK 240
QY 241 FEKIPVITPVVNDAPQTTSASVTLDVGVFGGEIGMRFTF 280
DB 241 FEKIPVITPVVNDAPQTTSASVTLDVGVFGGEIGMRFTF 280

RESULT 9

US-10-901-714-48
; Sequence 48, Application US/10901714
; Publication No. US20040265334A1
; GENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
; APPLICANT: OHASHI, NORIO
; TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRlichia CANIS AND EHRlichia
; FILE REFERENCE: 22727-04109
; CURRENT APPLICATION NUMBER: US/10/901,714
; CURRENT FILING DATE: 2004-07-29
; PRIOR FILING DATE: 09/314,701
; PRIOR APPLICATION NUMBER: 60/100,843
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 48

; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-10-901-714-48
Query Match 100.0%; Score 1462; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 9.8e-136;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKEGFYISAKYNPSISHPRKFSABET 60
DB 1 MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKEGFYISAKYNPSISHPRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKDGDITKKDDFTRVAPGIDFQNNLISGFGSGISYMDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKDGDITKKDDFTRVAPGIDFQNNLISGFGSGISYMDGPRIELE 120
QY 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAMEDQQYVVLKNDGITTMSLMVNTCYDIT 180
DB 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAMEDQQYVVLKNDGITTMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIADLITIFKDLNLFKPAYQKGIGISYPITPEVSATFYGYYHGVGNK 240
DB 181 AEGVSFVPYACAGIADLITIFKDLNLFKPAYQKGIGISYPITPEVSATFYGYYHGVGNK 240
QY 241 FEKIPVITPVVNDAPQTTSASVTLDVGVFGGEIGMRFTF 280
DB 241 FEKIPVITPVVNDAPQTTSASVTLDVGVFGGEIGMRFTF 280

RESULT 10

US-10-901-774-48
; Sequence 48, Application US/10901774
; Publication No. US20040265334A1
; GENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
; APPLICANT: OHASHI, NORIO
; TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRlichia CANIS AND EHRlichia
; FILE REFERENCE: 22727-04109
; CURRENT APPLICATION NUMBER: US/10/901,774
; CURRENT FILING DATE: 2004-07-29
; PRIOR FILING DATE: 09/314,701
; PRIOR APPLICATION NUMBER: 60/100,843
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-10-901-774-48

Query Match 100.0%; Score 1462; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 9.8e-136;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKEGFYISAKYNPSISHPRKFSABET 60
DB 1 MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKEGFYISAKYNPSISHPRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKDGDITKKDDFTRVAPGIDFQNNLISGFGSGISYMDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKDGDITKKDDFTRVAPGIDFQNNLISGFGSGISYMDGPRIELE 120
QY 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAMEDQQYVVLKNDGITTMSLMVNTCYDIT 180
DB 121 AAYQQFNPKNNTDNDNGEYKHFALSRKDAMEDQQYVVLKNDGITTMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIADLITIFKDLNLFKPAYQKGIGISYPITPEVSATFYGYYHGVGNK 240
DB 181 AEGVSFVPYACAGIADLITIFKDLNLFKPAYQKGIGISYPITPEVSATFYGYYHGVGNK 240

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QY 241 FEKIPVITPVVNDAPQTTASVTLVDVYFGGEGIGMRFTF 280
Db 241 FEKIPVITPVVNDAPQTTASVTLVDVYFGGEGIGMRFTF 280

RESULT 11
US-09-846-808-14
; Sequence 14, Application US/09846808
; Patent No. US20020064531A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: Yu, Xu-Jie
; TITLE OF INVENTION: Ehrlichia chaffeensis 28 kDa Outer Membrane
; TITLE OF INVENTION: Protein Multigene Family
; FILE REFERENCE: D6311
; CURRENT APPLICATION NUMBER: US/09/846,808
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/201,035
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 53
; SEQ ID NO 14
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: P28-14 Outer Membrane Protein of
; OTHER INFORMATION: Ehrlichia chaffeensis
US-09-846-808-14

Query Match      82.3%; Score 1202.5; DB 3; Length 283;
Best Local Similarity 79.5%; Pred. No. 4.4e-110;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

QY 1 MNYKKILVRSALISLMSILPYQSPADPVGSR---TNDNKEGFIYSAKYNPSISHFRKFS 57
Db 1 MNYKKIFVSSALISLMSILPYQSPADPVTSNDTGTINDSREGFYISVKYNPSISHFRKFS 60

QY 58 EETPINGTNSLTKKVFGKKGGDITKKDDFTVRVAPGIDFQNNLISGFSIGYSMDGPRI 117
Db 61 EEAAYQQFNPKNNTDNGEYKHFALSRKDMEDQQVYVVKNDGITFMSLMWNTCY 120

QY 118 ELEAAQQFNPKNNTDNGEYKHFALSRKDMEDQQVYVVKNDGITFMSLMWNTCY 177
Db 121 ELEAAQKFDKPNNDNTNSGDYKYFGLSREDIAADKKYVVLKNEGITFMSLMWNTCY 180

QY 178 DITAEVGSFVPVACAGIGADLITIFKDLNLKFAYQGGKIGISYPTTPEVSAPFYGYYHGVI 237
Db 181 DITAEVGFPIPYACAGVADLNVFKNLKFYSQGGKIGISYPTTPEVSAPFYGYYHGVI 240

QY 238 GKNFEKIPVITPVVNDAPQTTASVTLVDVYFGGEGIGMRFTF 280
Db 241 GNNFNKIPVITPVVLEGAQTTSALVTIDTGYFGGEGVGRFTF 283

RESULT 12
US-09-811-007-10
; Sequence 10, Application US/09811007
; Publication No. US20030185849A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xu-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/811,007
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/201,035
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 10
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
US-09-811-007-10

Query Match      82.3%; Score 1202.5; DB 4; Length 283;
Best Local Similarity 79.5%; Pred. No. 4.4e-110;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

QY 1 MNYKKILVRSALISLMSILPYQSPADPVGSR---TNDNKEGFIYSAKYNPSISHFRKFS 57
Db 1 MNYKKIFVSSALISLMSILPYQSPADPVTSNDTGTINDSREGFYISVKYNPSISHFRKFS 60

QY 58 EETPINGTNSLTKKVFGKKGGDITKKDDFTVRVAPGIDFQNNLISGFSIGYSMDGPRI 117
Db 61 EEAAYQQFNPKNNTDNGEYKHFALSRKDMEDQQVYVVKNDGITFMSLMWNTCY 120

QY 118 ELEAAQQFNPKNNTDNGEYKHFALSRKDMEDQQVYVVKNDGITFMSLMWNTCY 177
Db 121 ELEAAQKFDKPNNDNTNSGDYKYFGLSREDIAADKKYVVLKNEGITFMSLMWNTCY 180

QY 178 DITAEVGSFVPVACAGIGADLITIFKDLNLKFAYQGGKIGISYPTTPEVSAPFYGYYHGVI 237
Db 181 DITAEVGFPIPYACAGVADLNVFKNLKFYSQGGKIGISYPTTPEVSAPFYGYYHGVI 240

QY 238 GKNFEKIPVITPVVNDAPQTTASVTLVDVYFGGEGIGMRFTF 280
Db 241 GNNFNKIPVITPVVLEGAQTTSALVTIDTGYFGGEGVGRFTF 283

RESULT 13
US-10-062-624-10
; Sequence 10, Application US/10062624
; Publication No. US20020115840A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xu-Jie
; TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2/D1
; CURRENT APPLICATION NUMBER: US/10/062,624
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 10
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
US-10-062-624-10

Query Match      82.3%; Score 1202.5; DB 4; Length 283;
Best Local Similarity 79.5%; Pred. No. 4.4e-110;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

QY 1 MNYKKILVRSALISLMSILPYQSPADPVGSR---TNDNKEGFIYSAKYNPSISHFRKFS 57
Db 1 MNYKKIFVSSALISLMSILPYQSPADPVTSNDTGTINDSREGFYISVKYNPSISHFRKFS 60

QY 58 EETPINGTNSLTKKVFGKKGGDITKKDDFTVRVAPGIDFQNNLISGFSIGYSMDGPRI 117
Db 61 EEAAYQQFNPKNNTDNGEYKHFALSRKDMEDQQVYVVKNDGITFMSLMWNTCY 120

QY 118 ELEAAQQFNPKNNTDNGEYKHFALSRKDMEDQQVYVVKNDGITFMSLMWNTCY 177
Db 121 ELEAAQKFDKPNNDNTNSGDYKYFGLSREDIAADKKYVVLKNEGITFMSLMWNTCY 180

QY 178 DITAEVGSFVPVACAGIGADLITIFKDLNLKFAYQGGKIGISYPTTPEVSAPFYGYYHGVI 237
Db 181 DITAEVGFPIPYACAGVADLNVFKNLKFYSQGGKIGISYPTTPEVSAPFYGYYHGVI 240

QY 238 GKNFEKIPVITPVVNDAPQTTASVTLVDVYFGGEGIGMRFTF 280
Db 241 GNNFNKIPVITPVVLEGAQTTSALVTIDTGYFGGEGVGRFTF 283

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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:47:54 ; Search time 31.1111 Seconds
(without alignments)
91.208 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462

Sequence: 1 MYKKILVRSALISLSILP.....ASVTLDVGFGGICMRFTF 280

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70609 seqs, 10134256 residues

Total number of hits satisfying chosen parameters: 70609

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93.5	6.4	658	US-10-873-528-17	Sequence 17, Appl
2	93.5	6.4	677	US-10-873-528-155	Sequence 155, Appl
3	89.5	6.1	1288	US-11-052-554A-93	Sequence 93, Appl
4	87.5	6.0	669	US-10-997-201A-30	Sequence 30, Appl
5	87.5	6.0	1255	US-11-052-554A-271	Sequence 271, Appl
6	87.5	6.0	1255	US-11-052-554A-272	Sequence 272, Appl
7	86	5.9	657	US-10-957-880-4	Sequence 4, Appl
8	86	5.9	1255	US-11-022-562-235	Sequence 235, Appl
9	86	5.9	1255	US-11-052-554A-265	Sequence 265, Appl
10	86	5.9	1255	US-11-052-554A-266	Sequence 266, Appl
11	86	5.9	1255	US-11-052-554A-267	Sequence 267, Appl
12	86	5.9	1255	US-11-052-554A-268	Sequence 268, Appl
13	86	5.9	1255	US-11-052-554A-269	Sequence 269, Appl
14	86	5.9	1255	US-11-052-554A-270	Sequence 270, Appl
15	86	5.9	1255	US-11-052-554A-273	Sequence 273, Appl
16	86	5.9	1255	US-11-052-554A-274	Sequence 274, Appl
17	86	5.9	1255	US-11-052-554A-275	Sequence 275, Appl
18	86	5.9	1279	US-10-957-880-3	Sequence 3, Appl
19	84	5.7	1123	US-11-037-243-77	Sequence 77, Appl
20	81.5	5.6	628	US-11-080-991-108	Sequence 108, Appl
21	79.5	5.4	1296	US-10-615-668-3	Sequence 3, Appl
22	79.5	5.4	2367	US-11-051-453-42	Sequence 42, Appl
23	79	5.4	1458	US-11-096-274-2	Sequence 2, Appl
24	78.5	5.4	423	US-11-167-856-8	Sequence 8, Appl
25	78.5	5.4	2516	US-10-647-956A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-873-528-17
; Sequence 17, Application US/10873528
; Publication No. US2005027681A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129W0
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-17

Query Match 6.4%; Score 93.5; DB 6; Length 658;
Best Local Similarity 22.5%; Pred No. 0.86; Mismatches 92; Indels 37; Gaps 10;

Matches	47;	Conservative	33;
Query	73	FKLKGDDITKK-----DDFTRV-----APGIDFQNNLISGFS-GSIGYSMDGPRIELEAA	122
Db	328	FYLSKSDGKIAEKEMWYVSHSQAWYFKGGYMAKNETVDGYQLGSDGKWLGCKTTNENAA	387
Query	123	YQFNPKNITDNDTNGEYKHFALSR-----KDAMEDQYVVLKNDGIT-FMSLMWNTC	176
Db	388	YQVVPVTVANVYDS-GEKLSYISQGSVVWLDKDKSDKRLAITISLGSYMK-----T	441
Query	177	YDITAEGVS--FVPYACAGIGADLITPKDLNKLKAYQGGKIGISYPITPEVSAP-IGGY	233
Db	442	EDLQALDASKDIPY-----YESGHRFYHYVAQNASIPVASHLSDMVEGKXY	489
Query	234	HGVIGNKFEKIPVITPVVVLNDAPQTTAS	262
Db	490	YSADGLHFDGFKLENPFLFKDLTEATNYS	518

RESULT 2

[illegible]

RESULT 8
US-11-022-562-235
; Sequence 235, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27

Qy	42	SAKNPS-I\$HFKESAETPINGNSLTKKVFGGLKKGGDITKDKDDFTKVAEG-----ID	95
Dd	353	SVLNSTFSTFKCYGVGATKLN---DLCSFNYYA---DSFVYKGDDVRQIAPQGTCGTAD	407
Qy	96	FONNLISGFSGSIGYSMDGPRIELEAAVQQENPKNTDNNDTNGEY-KYHFALSRKDAME	154
Dd	408	YNYKLPDDFMGCV-----LAMNTRNIDATSTGNYNKYRLRHGKLRPPE	452
Qy	155	-DOOYVVVLKNDGITFMSLMVNITY-----DITAEGVSFVPYACAGIGADLIT-----	200
Dd	453	RDISNVPPSPDGKCPCTPALN-CYWPLNDYGFTTTTGICYQYPRVVLSFELLNAPATVC	511
Qy	201	-----IFKOLNKFAQYQKIGISYPITPEVSAP	228
Dd	512	GPKLSTDLIKQCVCNFNFNGLTGTGV-LTPSSKRFF	545

RESULT 12
US-11-052-554A-268
; Sequence 268, Application US/11052554A
; Publication No. US20050288666A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 268
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: SARS coronavirus TW1
US-11-052-554A-268

Query Match	5.9%;	Score 86;	DB 7;	Length 1255;
Best Local Similarity	21.4%;	Pred. No. 9.6;		
Matches	46;	Conservative	27;	Mismatches 92; Indels 50; Gaps 11;
<hr/>				
Qy	42	SAKNPS-IGHFRKFSABETPI	NGTSLTKVKFGLKKGDIT	TKDDTRVAPG-----ID 95
Db	353	SVLYNSTFFSTFKYGSATKLN-	DLCFSNYA--DSFPVKGD	VQRATPGGTGIAD 407
<hr/>				
Qy	96	FQNNLISGFSIGSYMGDPRIE	AAYQQFNPKNTDNDNGEY-	YKHFAJSRKDAME 154
Db	408	YNYKLPDPDFMGCV-----	LAWNTRNIDATSGTYNYKYR	LRLHGKLRPFE 452
<hr/>				
Qy	155	-DQOYVVVLKNDGITFMSLW	NVTCTY-----DITAEGVS	FVPYCAGIGADLLT- 200
Db	453	RDISNVSPDGKCTCPALN-C	WVPLNDGYFTTTTGIGYQP	IRVVVLSPPELLNAPTVC 511
<hr/>				
Qy	201	-----IFKDNLNKFYQGKI	GISYPITPEVSAP 228	
<hr/>				
Db	512	GPKLTDLIKNQCVNFNGIL	TGTGV-LTFSSKRPF 545	

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RESULT 13
US-11-052-554A-269
; Sequence 269, Application US/11052554A
; Publication No. US20050288666A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052.554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227

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; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 269
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: SARS coronavirus CUHK-Su10
US-11-052-554A-269

Query Match          5.9%; Score 86; DB 7; Length 1255;
Best Local Similarity 21.4%; Pred. No. 9.6;
Matches 46; Conservative 27; Mismatches 92; Indels 50; Gaps 11;

Qy 42 SAKYNPS-ISHFRKFSAEETPINGTNSLTKKVFGLKKDGDITKKDDFTRVAPG-----ID 95
Db 353 SVLYNSTFFSTFKCYGVSATKLN--DLCSNVVA---DSPVVKDDVRQIAPQGTGVIAD 407
Qy 96 FQNNLISGSGSGSYGSMGDGPRIEAAAYQFNPQNTDNDTNGEY-YKHFAIJSRKDAME 154
Db 408 YNYKLPDDPFMGCV-----LAWNTRNIDATSTGNYNYKYRYLRHGKLRPFE 452
Qy 155 -DQQYVVLKNDGITFMSLMVNTCY-----DITAEGSVPVPVACAGIGADLIT----- 200
Db 453 RDISNVFFSPDGKCTFPALN-CYWLNDYGFYTTTGIGYQPIRVVVLSPFLNAPATVC 511
Qy 201 -----IFKDLNLKFAYQKGIGISYPIITPEVSAP 228
Db 512 GPKLSTDLIKNQCVNFNGLTGTGV-LTPSSKRF 545

RESULT 14
US-11-052-554A-270
; Sequence 270, Application US/11052554A
; Publication No. US2005028866A1

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RESULT 14
US-11-052-554A-270
; Sequence 270, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 270
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: SARS coronavirus Urbani
US-11-052-554A-270

Query Match	5.9%	Score 86;	DB 7;	Length 1255;
Best Local Similarity	21.4%;	Pred. No. 9.6;		
Matches	46;	Conservative	27;	Mismatches 92; Indels 50; Gaps 11;
Qy	:	42	SAKYNPS-ISHRFKFSAEETPINGTNSLTKYKVGFLKKDGDITKKDDPFRVAPG----	ID 95
Db	:	353	SVLYNSTFFSTFKCYGVSAATKLN--DLCFSNVYA---DSPVVKGDDVRQIAPQGTGVIAD	407
Qy	:	96	FQNNLISGSGSIGYSMDGPRIEAAAYQOFNPKNTDNDTNDGEY-YKHFAFLSRKDAME	154
Db	:	408	YNYKLPDDFGVCV-----LAWNTRNIDATSTGNYNTKYRYLHRGKLRPFPE	452
Qy	:	155	-DQOYVVLKNDGITTFMSLMWNTCY-----DITAEGVSFVPVACAGIGADLIT-----	200
Db	:	453	RDISNVPFSDGPKCTPPALN-CYWPLNDYGFYTTTGIGYQYPVVVLSPFELLNAPATVC	511
Qy	:	201	-----IFKDLNLKFAYQCKIGISYPIITPEVSAF	228

Db 512 GPKLSTDLLKQCVNFNFNGLTGTGV-LTPSSKRF 545

RESULT 15

US-11-052-554A-273
; Sequence 273, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 273
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: SARS coronavirus GD01
US-11-052-554A-273

Query Match 5.9%; Score 86; DB 7; Length 1255;
Best Local Similarity 21.4%; Pred. No. 9.6;
Matches 46; Conservative 27; Mismatches 92; Indels 50; Gaps 11;
QY 42 SAKYNPS-ISHPRKFSAEETPINGTNSLTKKVFLKKGDDITKDDPTTRVAPG-----ID 95
Db 353 SVLYNSTPFTPKCYGVSA TKLN--DLCFSNVYA---DSFVVKGGDDVRQIAPGQTGVAD 407
QY 96 FQNNLISGFSIGYSGMDGPRIELEAAVQQFNPKNKTNNDDTNGEY-YKHFAFSRDKAME 154
Db 408 YNYKLDPDFMGCV-----LAWNTRIDATSTGNYNKYRYLRHGLRPF 452
QY 155 -DQYVVLKNDGITFMSLMVNTCY-----DITAEVSVFVPYACAGIGADLIT----- 200
Db 453 RDISNVVPSDGGKCTPPALN-CYWLNDYGFYTTTGIGYQPYRVVLSYELLNAPATV 511
QY 201 -----IPKDLNLKPAYOGKIGISYPTPEVSAF 228
Db 512 GPKLSTDLLKQCVNFNFNGLTGTGV-LTPSSKRF 545

Search completed: January 24, 2006, 12:04:18
Job time : 31.1111 secs

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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:36:23 ; Search time 43.9216 Seconds
(without alignments)
613.382 Million cell updates/sec

Title: US-10-680-349-42
Perfect score: 1462
Sequence: 1 MNYKKILVRSALISLMSILP.....ASVTLDVGVGGEIGMRFTF 280
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629.5	43.1	276	JE0218	28k surface artige
2	620	42.4	286	JE0219	28k surface artige
3	603	41.2	280	JE0217	28k surface artige
4	583	39.9	278	JE0216	28k surface artige
5	565	38.6	284	2 I40882	major antigenic pr
6	515.5	35.3	287	JE0220	28k surface artige
7	386.5	26.4	282	I39648	major surface prot
8	227.5	15.6	133	JE0221	28k surface artige
9	119.5	8.2	264	I54668	heat resistant agg
10	107.5	7.4	239	AH0541	probable outer mem
11	104.5	7.1	738	S01892	hemolysin A precur
12	102	7.0	1176	A27826	DNA-directed RNA p
13	101.5	6.9	415	B70448	3-oxoacyl-[acyl-ca
14	100	6.8	1582	AC1153	adhesin homolog lm
15	98	6.7	3890	C89921	hypothetical prote
16	97.5	6.7	274	AC3295	heat resistant agg
17	97.5	6.7	1174	S28976	DNA-directed RNA p
18	97.5	6.7	1271	A45555	glutamate rich pro
19	97.5	6.7	1310	AD1380	glycosidase homolo
20	95	6.5	1004	B25039	outer cell wall pr
21	95	6.5	1578	AD1512	peptidoglycan boun
22	94.5	6.5	474	F97264	6-Phospho-Beta-D-G
23	93.5	6.4	658	E95111	endo-beta-N-acetyl
24	93	6.4	180	F71639	hypothetical prote
25	93	6.4	608	H64473	hypothetical prote
26	93	6.4	745	T51370	hypothetical prote
27	92.5	6.3	219	AF2658	conserved hypotet
28	92.5	6.3	219	C97440	hypothetical prote
29	92.5	6.3	401	F86754	prophage p12 prote

30 92.5 6.3 585 2 C69336 probable electron
31 91.5 6.3 721 2 C97980 endo-beta-N-acetyl
32 91.5 6.3 1224 2 A25884 DNA-directed RNA p
33 91.5 6.3 1635 2 AI0452 hemolysin [importe
34 91 6.2 282 2 S16617 opacity protein op
35 91 6.2 588 2 AG0517 penicillin-binding
36 91 6.2 1348 2 B23496 TyB protein - yeas
37 91 6.2 1598 2 S69967 TyB protein - yeas
38 91 6.2 1770 2 S69953 TyB protein - yeas
39 91 6.2 1770 2 S58651 TyB protein - yeas
40 91 6.2 1770 2 S70233 TyB protein - yeas
41 91 6.2 1770 2 S69966 TyB protein - yeas
42 91 6.2 1770 2 S70230 TyB protein - yeas
43 91 6.2 1770 2 S69950 TyB protein - yeas
44 91 6.2 1771 2 S53592 TyB protein - yeas
45 91 6.2 1810 2 S69973 TyB protein - yeas

ALIGNMENTS

RESULT 1
JE0218
28k surface antigen 5 - Ehrlichia chaffensis
N:Alternate names: MAP1
C:Species: Ehrlichia chaffensis
C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C:Accession: JE0218
R:Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A:Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe i
A:Reference number: JE0216; MUID:98321180; PMID:9647746
A:Accession: JE0218
A:Molecule type: DNA
A:Residues: 1-276 <RED>
A:Cross-references: UNIPROT:Q93DD2; UNIPROT:Q9AC19; UNIPARC:UPI000003478F; GB:AF062761

Query Match 43.1%; Score 629.5; DB 2; Length 276;
Best Local Similarity 47.9%; Pred. No. 5.4e-44;
Matches 137; Conservative 41; Mismatches 87; Indels 21; Gaps 6;

QY 1 MNYKKILVRSALISLMSILPYOSPADPVGSRNDNKNKGFIYISAKYNPSISHPRKFSABET 60
DB 1 MNYKKVFTTSALISLISLPGVSFSDPAGSGINGN---FYISGKYMPSASHRGVFSAKE- 56
QY 61 PINGTNSLTKKYFGLKKDQD-----ITKKDFTVAPGIDFQNNLISGFSGSGVSM DG 114
DB 57 ----BRNTTVGVGFLKQNWDSAINSSPNDVFTVSNYSFKYENNPFLGFAIGVSM DG 112
QY 115 PRIELEAAYQQPNPKNTDNDNGEYKHFALSRLKDAME----DQYVVLKNDGITTFS 170
DB 113 PRIELEVSVEYTFDVKQGN--YKNEAHRVCALSHNSAADMSASNNFVFLKNEGLLDIS 170
QY 171 LMVNTCYDITAGVSFVPYACAGIGADLITIPKDLNLPAYOGKIGISVPIPEVSAPFG 230
DB 171 FMLNACYDVGSGIPFSPYICAGIGTDLVMEFATNPKISYQKGLGSLYSISPEASVFIG 230
QY 231 GYVHGVIQKBEKIPVITPVVLNDAPO--TTSASVTLDDVGVFGGEIG 275
DB 231 GHFHKVIQNEFRDIPITLTGTSLAGKNYPVAILVDVCHFGIEMG 276

RESULT 2
JE0219
28k surface antigen 2 - Ehrlichia chaffensis
N:Alternate names: MAP1
C:Species: Ehrlichia chaffensis
C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C:Accession: JE0219
R:Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A:Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe i
A:Reference number: JE0216; MUID:98321180; PMID:9647746

[illegible]

Matches 96; Conservative 54; Mismatches 113; Indels 35; Gaps 9;

Qy 1 MNVKKIL---VRSLISLMSILPYQS-FADP-----VGSRTNDNKEGFYISAKYN---PSI 49
|||::: : : : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1 MNVRELTGGLSANTVCACSLLVSGAVVASPWSEHVASEGVMGGSPFVGAAYSFAFSV 60
50 SHP--RKPSABETPINGNSLTKKVLGDKGDITKKDDFTRVAPGIDFQNNLISGFSGS 107
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 61 TSFDMRESSKETSVRGYDKSIATI-----DVSVPANFSKSGYTFAFSKNLITSFDGA 113
108 IGYSMQDPRIELEAYQQFNPKNTDNNDTNGEYYKH-----FALSRRKDAMEDQQVVVK 162
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 114 VGSLSGARVELEYSRRP-----ATLDGVQAKSAGESLAATRANITETNYFVVK 166
163 NDIITFMSLMVTNCYDTAEGVSPVPACAGIGADLIITFKDLNLKFAYOGKIGISYPT 222
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 167 IDEITNTSVMLNGCYDVHLTDLPSPYPYCAGIGASFVDISKQVTTKLAYRKGVISQFT 226
223 PEVSATFGYYHGVIQGNKEFIPIVTPVWLNDAPQTTSASVTLDVDYGFEIGMRPTF 280
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 227 PETSLVAGGFPHGLFDESXKDIPAHNSVKFSG--EAKASVKAHTADYGFNLGARPLF 281

RESULT 8
JE0221
C:Species: Ehrlichia canis
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C:Accession: JE0221
R;Reddy, G.R.; Sulisana, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe I
A;Reference number: JE0216; MUID:983221180; PMID:9647746
A;Accession: JE0221
A:Molecule type: DNA
A;Residues: 1-133 <RED>
A;Cross-references: UNIPROT:O85360; UNIPARC:UI0000034791; GB:AF062762; NID:g3327964; PII

Query Match 15.6%; Score 227.5; DB 2; Length 133;
Best Local Similarity 41.4%; Pred. No. 1.4e-11;
Matches 58; Conservative 20; Mismatches 49; Indels 13; Gaps 4;

Qy 1 MNVKKILVRSLISLMSILPYQSPADPVGSRNDNKEGFYISAKYNPSISHFRKESAERT 60
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 1 MNCKKVFTISALISSIYFLPNVSYSNPYG--NSMYGNFYISGKYMPSPVPHGFIFSABE- 57
61 PINGTNSLTKKVFGLKGD--GDI-----TKDDFTRVAPGIDFQNNLISGFSGSIGYMDG 114
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 58 -----EKKKTIVVYLKENWAGDAISSQSPDDNFTRINSFKYASNKFLGFAVAIGSYS 113
115 PRIELEAYQQFNPKNTDNN 134
||||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 114 PRIEVENSYEAFDVKNQGN 133

RESULT 9
I54668
Heat resistant agglutinin 1 - Escherichia coli
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I54668; I69133; I69134
R;Lutwyche, P.; Rupps, R.; Cavanagh, J.; Warren, R.A.; Brooks, D.E.
Infect. Immun. 62, 5020-5026, 1994
A;Title: Cloning, sequencing, and viscometric adhesion analysis of heat-resistant aggluti
A;Reference number: I54668; MUID:95012721; PMID:7927783
A;Accession: I54668
A;Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-264 <RES>
A;Cross-references: UNIPROT:Q46678; UNIPARC:UI000008BES5A; EMBL:U07174; NID:g463910; PII
A;Accession: I69133
A;Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA

			6.9%;	Score 101.5;	DB 2;	Length 415;	
			Best Local Similarity 21.7%;	Pred. No. 1.3;			
			Matches 60;	Conservative 32;	Mismatches 73;	Indels 111;	GapØ 14;
Qy	62	INGTNSLTKVFLGKDGDTKKDDFTRVAPGDIFQNLLISGFSG-----SIGYSMDGPR	116				
	: :	: :					
Db	7	ITGIGAVTPLGTGVKK-----FWENLVKGYSGVDYIKSFNPDEYGIP	48				
Qy	117	IIELEAAVQQFNPKV-TDNNDTDNGEYYKHFAISR-KDAMED-----	155				
	: : : : :	: : : : :	: : :				
Db	49	VKTAAEVKDFNPFDMFKKEARKASRFVQPAIAAVKEALSDGLISEYDPYRVGIIGT	108				

A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89921
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-3890 <KUR>
A:Cross-references: UNIPROT:Q99U53; UNIPARC:UPI00000CAB07; GB:BA000018; PID:gl3701233; H
A:Experimental source: strain N315
C:Genetics:
A:Gene: ebhB

Query Match	6.7%;	Score 98;	DB 2;	Length 3890;
Best Local Similarity	22.3%;	Pred. No. 47;		
Matches	65;	Conservative 48;	Mismatches 114;	Indels 64; Gaps 14;

QY	3	YKKILVRSALISLMSILPYQ----	SPADPVGSRSTNDNKEGFIYISAKYNPSISHFRKFSABE	59
Db	892	YNKV-VASNMSNAVTILPDDIPPTINPVG-----	INAKY-----YRGDE	930
QY	60	TPINGTNSLTKKVGLKKGDITKKDDPTRVAPGIDFQNNLISGFSGSIGYSMDGPRIEL	119	
Db	931	--VNFTMGVSDRHSIGIKNTTITLPSGWTSNLTKSDNKN-----	GSLAIT---GRVSM	978
QY	120	EAAVQQ---FNPKNITDN-NDTDNGEYKHFALSRKXDAVEDQQYVVLKNDGITFMSLMVNT	175	
Db	979	NQAFNSDITFKVSATDNVNTTNDQSQKHVSIHVCKISEDAHPIVLGN---	TEKVVVVNP	1035
QY	176	CYDITARGVSFVPYACAGIGADLIITFKDLNLKFAYQKIGISYPITPEVSAFIGGYHYG	235	
Db	1036	TAVSDEKQS-----IITAFMNKNQNI--RGLASTDPVTVDNNGNVTLHYRD	1081	
QY	236	VIGNKFEKIPVIT--PVVLND-----APQTTASVTLDVGYFGGEIGHRET	279	
Db	1082	GSSTTLDATNVMTYBFWVKSEYQTANAAKTATVTIAKGOSFNIGDIKQYFT	1132	

Search completed: January 24, 2006, 11:47:47
Job time : 45.9216 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:35:23 ; Search time 210.458 Seconds
(without alignments)
938.659 Million cell updates/sec

Title: US-10-680-349-42
Perfect score: 1462
Sequence: 1 MNYKILVRSALISLMSILP.....ASVTLDVGFGEIGMRFTF 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1462	100.0	280	2	Q9F476_EHRCA	Q9f476 ehrlichia c
2	1452	99.3	280	2	Q84HUI_EHRCA	Q84hui ehrlichia c
3	1224.5	83.8	283	2	Q8G8D6_EHRCH	Q8g8d6 ehrlichia c
4	1217.5	83.3	283	2	Q8G8I2_EHRCH	Q8g8i2 ehrlichia c
5	1217.5	83.3	283	2	Q8G8U4_EHRCH	Q8g8u4 ehrlichia c
6	1202.5	82.3	283	2	Q8S358_EHRCH	Q8s358 ehrlichia c
7	1124	76.9	282	2	Q9R443_EHRRU	Q9r443 ehrlichia r
8	1123	76.8	282	2	Q5W5Y1_EHRRU	Q5w5y1 ehrlichia r
9	1121	76.7	282	2	Q4LOCO_EHRRU	Q4loco ehrlichia r
10	1121	76.7	304	2	Q5FGL4_EHRRG	Q5fgl4 ehrlichia r
11	1121	76.7	304	2	Q5PCD9_EHRRW	Q5pcd9 ehrlichia r
12	1120	76.6	282	2	Q5HA10_EHRRW	Q5ha10 ehrlichia r
13	1120	76.6	282	2	Q9WW41_EHRRU	Q9ww41 ehrlichia r
14	665.5	45.5	275	2	Q93DD4_EHRCH	Q93dd4 ehrlichia c
15	655	44.8	276	2	Q8G8U0_EHRCH	Q8g8u0 ehrlichia c
16	651	44.5	276	2	Q8S817_EHRCH	Q8s817 ehrlichia c
17	648	44.3	280	2	Q9ZGM9_EHRCH	Q9zgm9 ehrlichia c
18	647	44.3	276	2	Q93DD1_EHRCH	Q93dd1 ehrlichia c
19	645.5	44.2	281	2	Q93DD2_EHRCH	Q93dd2 ehrlichia c
20	644.5	44.1	281	2	Q9AC19_EHRCH	Q9ac19 ehrlichia c
21	644	44.0	280	2	Q8S816_EHRCH	Q8s816 ehrlichia c
22	628	43.0	280	2	Q93DD3_EHRCH	Q93dd3 ehrlichia c
23	621	42.5	288	2	Q9ZGJ2_EHRCA	Q9zgj2 ehrlichia c
24	620	42.4	286	2	Q93DD5_EHRCH	Q93dd5 ehrlichia c
25	605	41.4	291	2	Q52107_EHRCH	Q52107 ehrlichia c
26	605	41.4	291	2	Q8G8P3_EHRCH	Q8g8p3 ehrlichia c
27	601	41.1	280	2	Q9ADV3_EHRCA	Q9adv3 ehrlichia c
28	600	41.0	280	2	Q9F473_EHRCA	Q9f473 ehrlichia c
29	599	41.0	291	2	Q8G921_EHRCH	Q8g921 ehrlichia c
30	598	40.9	291	2	Q8GGU2_EHRCH	Q8ggu2 ehrlichia c
31	592	40.5	285	2	Q9L6Y5_EHRCH	Q9l6y5 ehrlichia c

32	589	40.3	287	2	Q8GGU3_EHRCH	Q8ggug3 ehrlichia c
33	588	40.2	278	2	Q9R3J3_EHRCA	Q9r3j3 ehrlichia c
34	588	40.2	278	2	Q9R8A5_EHRCA	Q9r8a5 ehrlichia c
35	588	40.2	278	2	Q9R8A6_EHRCA	Q9r8a6 ehrlichia c
36	588	40.2	278	2	Q9R8A7_EHRCA	Q9r8a7 ehrlichia c
37	588	40.2	278	2	Q9R8A8_EHRCA	Q9r8a8 ehrlichia c
38	588	40.2	278	2	Q9R8A9_EHRCA	Q9r8a9 ehrlichia c
39	588	40.2	307	2	Q9ZGJ1_EHRCA	Q9zgj1 ehrlichia c
40	583.5	39.9	277	2	Q8G8W7_EHRCH	Q8g8w7 ehrlichia c
41	583.5	39.9	277	2	Q8GGU1_EHRCH	Q8ggug1 ehrlichia c
42	583	39.9	278	2	Q9F472_EHRCA	Q9f472 ehrlichia c
43	583	39.9	278	2	O52106_EHRCH	O52106 ehrlichia c
44	573.5	39.2	279	2	Q8G8Q1_EHRCH	Q8g8q1 ehrlichia c
45	573.5	39.2	282	2	Q4W4X0_EHRRU	Q4w4x0 ehrlichia r

ALIGNMENTS

RESULT 1
Q9F476_EHRCA
ID Q9F476_EHRCA PRELIMINARY; PRT; 280 AA.
AC Q9F476_EHRCA
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE P28-2 (Major outer membrane protein p30-10)
DE P28-2 (Major outer membrane protein p30-10)
GN Name=p28-2; Synonyms=p30-10;
OS Ehrlichia canis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=944;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Jake;
RX MEDLINE=99242757; PubMed=10225842;
RA McBride J.W., Yu X.J., Walker D.H.;
RT "Molecular cloning of the gene for a conserved major immunoreactive
RT 28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
RT antigen.";
RL Clin. Diagn. Lab. Immunol. 6:392-399(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Jake;
RX MEDLINE=20432107; PubMed=10974556; DOI=10.1016/S0378-1119(00)00256-0;
RA McBride J.W., Yu X.J., Walker D.H.;
RT "A conserved, transcriptionally active p28 multigene locus of
RT Ehrlichia canis.";
RL Gene 254:245-252(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Oklahoma;
RX MEDLINE=98371112; PubMed=9705412;
RA Ohashi N., Unver A., Zhi N., Rikihisa Y.;
RT "Cloning and characterization of multigenes encoding the
RT immunodominant 30-kilodalton major outer membrane proteins of
RT Ehrlichia canis and application of the recombinant protein for
RT serodiagnosis.";
RL J. Clin. Microbiol. 36:2671-2680(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Oklahoma;
RX MEDLINE=21153566; PubMed=11254561;
RA DOI=10.1128/IAI.69.4.2083-2091.2001;
RT "Analysis of transcriptionally active gene clusters of major outer
RT membrane protein multigene family in Ehrlichia canis and E.
RT chaffeensis.";
RL Infect. Immun. 69:2083-2091(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Venezuela, Arizona, California, and New Mexico;
RX MEDLINE=22461952; PubMed=12574308; DOI=10.1128/JCM.41.2.886-888.2003;

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RA Felek S., Greene R., Rikihisa Y.;
RT "Transcriptional Analysis of p30 Major Outer Membrane Protein Genes of
RT Ehrlichia canis in Naturally Infected Ticks and Sequence Analysis of
RT p30-10 of E. canis from Diverse Geographic Regions.";
RL J. Clin. Microbiol. 41:886-888(2003).
DR EMBL; AF082744; AAG14357.1; -; Genomic DNA.
DR EMBL; AF078553; AAK28696.1; -; Genomic DNA.
DR EMBL; AF324792; AAK31312.1; -; Genomic DNA.
DR EMBL; AF528512; AAO41109.1; -; Genomic DNA.
DR EMBL; AF528515; AAO41112.1; -; Genomic DNA.
DR EMBL; AF528514; AAO41111.1; -; Genomic DNA.
DR EMBL; AF528511; AAO41108.1; -; Genomic DNA.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 280 AA; 30962 MW; D1BB28B5AF0E6CA3 CRC64;

Query Match 100.0%; Score 1462; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 5,3e-108;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYKKILVRSALISLSILPYQSFADPVGSRNTDNKKEGYISAKYNPSISHFRKFSABET 60
DB 1 MNYKKILVRSALISLSILPYQSFADPVGSRNTDNKKEGYISAKYNPSISHFRKFSABET 60

QY 61 PINGNTSLTKKVFGLKKGGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYMDGPRIELE 120
DB 61 PINGNTSLTKKVFGLKKGGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYMDGPRIELE 120

QY 121 AAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180

QY 121 AAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180

QY 181 AEGVSFVPYACAGIGADLITIFKDLNLKFPAYQKGIGISYPIPTPEVSFAFTGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIGADLITIFKDLNLKFPAYQKGIGISYPIPTPEVSFAFTGGYHGVGNK 240

QY 241 FEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280

Query Match 83.8%; Score 1224.5; DB 2; Length 283;
Best Local Similarity 81.6%; Pred. No. 4,1e-89;
Matches 231; Conservative 24; Mismatches 25; Indels 3; Gaps 1;

QY 1 MNYKKILVRSALISLSILPYQSFADPVGSR---TNDNKEGYISAKYNPSISHFRKFS 57
DB 1 MNYKKIFVRSALISLSILPYQSFADPVTNSDGTGINDSKEGYISVKYNPSISHFRKFS 60

QY 58 BETPINGNTSLTKKVFGLKKGGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYMDGPRI 117
DB 61 BETPINGNTSLTKKVFGLKKGGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYMDGPRI 120

QY 118 ELEAAAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCY 177
DB 121 ELEAAAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCY 180

QY 178 DITAGVSFVPYACAGIGADLITIFKDLNLKFPAYQKGIGISYPIPTPEVSFAFTGGYHGV 237
DB 181 DITAGVSFVPYACAGIGADLITIFKDLNLKFPAYQKGIGISYPIPTPEVSFAFTGGYHGV 240

QY 238 GNKPEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
DB 241 GNPNFKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 283

RESULT 4

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DB 1 MNYKKILVRSALISLSILPYQSFADPVGSRNTDNKKEGYISAKYNPSISHFRKFSABET 60
QY 61 PINGNTSLTKKVFGLKKGGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYMDGPRIELE 120
DB 61 PINGNTSLTKKVFGLKKGGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYMDGPRIELE 120
QY 121 AAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIGADLITIFKDLNLKFPAYQKGIGISYPIPTPEVSFAFTGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIGADLITIFKDLNLKFPAYQKGIGISYPIPTPEVSFAFTGGYHGVGNK 240
QY 241 FEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280

RESULT 3
Q88D6_EHRCH
ID Q88D6_EHRCH PRELIMINARY; PRT; 283 AA.
AC Q88D6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE 28kDa outer membrane protein gene 14.
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=945;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22384137; PubMed=12496165; DOI=10.1128/IAI.71.1.187-195.2003;
RA Cheng C., Paddock C.D., Ganta R.R.;
RT "Molecular heterogeneity of Ehrlichia chaffeensis isolates determined
RT by sequence analysis of the 28-kilodalton outer membrane protein genes
RT and other regions of the genome.";
RL Infect. Immun. 71:187-195(2003).
DR EMBL; AF479835; AAO12939.1; -; Genomic DNA.
DR EMBL; AF479836; AAO12944.1; -; Genomic DNA.
DR EMBL; AF479838; AAO12954.1; -; Genomic DNA.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 283 AA; 31090 MW; D5825DD4DC51C425 CRC64;

Query Match 83.8%; Score 1224.5; DB 2; Length 283;
Best Local Similarity 81.6%; Pred. No. 4,1e-89;
Matches 231; Conservative 24; Mismatches 25; Indels 3; Gaps 1;

QY 1 MNYKKILVRSALISLSILPYQSFADPVGSR---TNDNKEGYISAKYNPSISHFRKFS 57
DB 1 MNYKKIFVRSALISLSILPYQSFADPVTNSDGTGINDSKEGYISVKYNPSISHFRKFS 60

QY 58 BETPINGNTSLTKKVFGLKKGGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYMDGPRI 117
DB 61 BETPINGNTSLTKKVFGLKKGGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYMDGPRI 120

QY 118 ELEAAAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCY 177
DB 121 ELEAAAYQFPNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCY 180

QY 178 DITAGVSFVPYACAGIGADLITIFKDLNLKFPAYQKGIGISYPIPTPEVSFAFTGGYHGV 237
DB 181 DITAGVSFVPYACAGIGADLITIFKDLNLKFPAYQKGIGISYPIPTPEVSFAFTGGYHGV 240

QY 238 GNKPEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
DB 241 GNPNFKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 283

RESULT 4

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Q8G8I2_EHRCH
ID Q8G8I2_EHRCH PRELIMINARY; PRT; 283 AA.
AC Q8G8I2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE 28kDa outer membrane protein gene 14.
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=945;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22384137; PubMed=12496165; DOI=10.1128/IAI.71.1.187-195.2003;
RA Cheng C., Paddock C.D., Ganta R.R.;
RT "Molecular heterogeneity of Ehrlichia chaffeensis isolates determined
RT by sequence analysis of the 28-kilodalton outer membrane protein genes
RT and other regions of the genome.";
RL Infect. Immun. 71:187-195(2003).
DR EMBL; AF479839; AAO12959.1; -; Genomic DNA.
DR EMBL; AF479840; AAO12965.1; -; Genomic DNA.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 283 AA; 31069 MW; AEA8B2833E02631F CRC64;
Query Match 83.3%; Score 1217.5; DB 2; Length 283;
Best Local Similarity 80.9%; Pred. No. 1.5e-88;
Matches 229; Conservative 24; Mismatches 27; Indels 3; Gaps 1;
QY 1 MNYKKILVRSALISLSILPYQSFADPVGSR---TNDNKEGFYISAKYNPSISHFRKFS 57
DB 1 MNYKKIFVRSALISLSILPYQSFADPVTSNDTGINDSKEGFPYISVKYNPSISHFRKFS 60
QY 58 EETPINGTNSLTKKVFGKKGDIKKODFTRVAPGIDFQNNLISGFSIGSYMDGPRI 117
DB 61 EETPINGTALTATKKVFGKKGDIAGHGNFTRDPALEFQNNLISGFSIGSYAMDGPRI 120
QY 118 ELEAAVQQFNPKNTDNDNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMWNTCY 177
DB 121 ELEAAVQKEDAKNPDSNDTNSGDIYKFGLSRDADAKKYVVLKNEGITFMSLMWNTCY 180
QY 178 DITAEGVSPVPYACAGIGADLITIPKDLNLFAYQKIGISYPIPEVSAFYGYYHGV 237
DB 181 DITAEGVPPPIPVACAGIGADLINVDFNLKFSYQKIGISYPIPEVSAFYGYYHGV 240
QY 238 GNKFEKIPVITPVVLNDAPQTTSASVTLVDVYFGGEGIGMRFTF 280
DB 241 GNNFNKIPVITPVVLEGAPQTTSALTVIDTGYGGEVGIRFTF 283
RESULT 6
O85358_EHRCH
ID O85358_EHRCH PRELIMINARY; PRT; 283 AA.
AC O85358; O52103;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE 28kDa outer membrane protein gene 14 (Major outer membrane protein
DE OMP-1B).
GN Name=omp-1b;
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=945;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98321180; PubMed=9647746; DOI=10.1006/bbrc.1998.8844;
RA Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
RA Alleman A.R.;
RT "Molecular characterization of a 28 kDa surface antigen gene family of
RT the tribe Ehrlichiae.";
RL Biochem. Biophys. Res. Commun. 247:636-643(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22384137; PubMed=12496165; DOI=10.1128/IAI.71.1.187-195.2003;
RA Cheng C., Paddock C.D., Ganta R.R.;
RT "Molecular heterogeneity of Ehrlichia chaffeensis isolates determined
RT by sequence analysis of the 28-kilodalton outer membrane protein genes
RT and other regions of the genome.";
RL Infect. Immun. 71:187-195(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Cheng C., Paddock C.D., Ganta R.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Arkansas;
RX MEDLINE=98084465; PubMed=9423849;
RA Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
RT "Immunodominant major outer membrane proteins of Ehrlichia chaffeensis
RT are encoded by a polymorphic multigene family.";
RL Infect. Immun. 66:132-139(1998).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Arkansas;
RX MEDLINE=21153566; PubMed=11254561;
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RX DOI=10.1128/IAI.69.4.2083-2091.2001;
RA Ohashi N., Rikihisa Y., Unver A.;
RT "Analysis of transcriptionally active gene clusters of major outer
RT Membrane protein multigene family in Ehrlichia canis and E.
RT chaffeensis.";
RL Infect. Immun. 69:2083-2091(2001).
DR EMBL; AF479833; AAC02929.1; -; Genomic DNA.
DR EMBL; U72231; AAC02936.1; -; Genomic DNA.
DR EMBL; AF479834; AAC02933.1; -; Genomic DNA.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 283 AA; 31017 MW; DCBCF652B771C95D CRC64;

Query Match      82.3%; Score 1202.5; DB 2; Length 283;
Best Local Similarity 79.5%; Pred. No. 2.3e-87;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

QY 1 MNYKILVRSALISLMSILPYQSFADPVGSR--TNDNKEGFYISAKYNPSISHFRKFS 57
DB 1 MNYKILVRSALISLMSILPYQSFADPVTSNTGTGNSREGFYISVKYNPSISHFRKFS 60
QY 58 EETPINGTNSLTKKVFGGLKKGDDITKKDFTTRVAPGIDFQNNLISGFSIGYSMDGPRI 117
DB 61 EETPINGTNSLTKKVFGGLKKGDDITKKDFTTRVAPGIDFQNNLISGFSIGYSMDGPRI 120
QY 118 ELEAAQQQFNPKNTDNDNGEYKHFALSRKDAEDQQYVVLKNDGITFMSLMVNTCY 177
DB 121 ELEAAQQQFNPKNTDNDNGEYKHFALSRKDAEDQQYVVLKNDGITFMSLMVNTCY 180
QY 178 DITAEQVSPVPYACAGIGADLITIPKDLNLFAYQKIGISYPTPEVSFAFIGGYHGV 237
DB 181 DITAEQVSPVPYACAGIGADLITIPKDLNLFAYQKIGISYPTPEVSFAFIGGYHGV 240
QY 238 GNKPEKIPVITPVVLNDAPQTTASVTLDDVGFGEIGMRFTF 280
DB 241 GNKPEKIPVITPVVLNDAPQTTASVTLDDVGFGEIGMRFTF 283

RESULT 7
Q9R443 EHRRU PRELIMINARY; PRT; 282 AA.
AC Q9R443;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DE Major antigenic protein 1 like protein.
OS Ehrlichia ruminantium (Cowdria ruminantium).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=779;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Senegal;
RX PubMed=15995193; DOI=10.1128/JB.187.14.4782-4791.2005;
RA Bekker C.P., Postigo M., Taoufik A., Bell-Saki L., Ferraz C.,
RA Martinez D., Jongejan F.;
RT "Transcription Analysis of the Major Antigenic Protein 1 Multigene
RT Family of Three In Vitro-Cultured Ehrlichia ruminantium Isolates.";
RL J. Bacteriol. 187:4782-4791(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Senegal;
RA Bekker C.P.J., Taoufik A., Jongejan F.;
RA Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF319940; AAV54088.2; -; Genomic DNA.
SQ SEQUENCE 282 AA; 31097 MW; 3D619510E7393EBB CRC64;

Query Match      76.8%; Score 1123; DB 2; Length 282;
Best Local Similarity 76.0%; Pred. No. 4.9e-81;
Matches 215; Conservative 23; Mismatches 41; Indels 4; Gaps 2;

QY 1 MNYKILVRSALISLMSILPYQSFADPVGSR--TNDNKEGFYISAKYNPSISHFRKFS 57
DB 1 MNYKILVRSALISLMSILPYQSFADPVGSR--TNDNKEGFYISAKYNPSISHFRKFS 60
QY 58 EETPINGTNSLTKKVFGGLKKGDDITKKDFTTRVAPGIDFQNNLISGFSIGYSMDGPRI 117
DB 61 EETPINGTNSLTKKVFGGLKKGDDITKKDFTTRVAPGIDFQNNLISGFSIGYSMDGPRI 120
QY 118 ELEAAQQQFNPKNTDNDNGEYKHFALSRKDAEDQQYVVLKNDGITFMSLMVNTCY 177
DB 121 ELEAAQQQFNPKNTDNDNGEYKHFALSRKDAEDQQYVVLKNDGITFMSLMVNTCY 179
QY 178 DITAEQVSPVPYACAGIGADLITIPKDLNLFAYQKIGISYPTPEVSFAFIGGYHGV 237
DB 240 DITAEQVSPVPYACAGIGADLITIPKDLNLFAYQKIGISYPTPEVSFAFIGGYHGV 237

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Db      180 DITAGGVFPVPACAGIAGDLISIFDDINLKPAYQCKIGISVPIPTPEISAFIGGYHGV 239
Qy      238 GNKFEKIPVITPVLNDAPQTTASVTLTDVGYFGGIEIGMRFTF 280
Db      240 GNKYNKIPVKLPVTLTDAQOSTASVTLTDAGYFGGELGVRFTF 282

RESULT 9
Q4LQCO EHRRU
ID Q4LQCO EHRRU PRELIMINARY; PRT; 282 AA.
AC Q4LQCO
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Map1-1.
OS Ehrlichia ruminantium (Cowdria ruminantium).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=779;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Gardel.
RA Martinez D., Ferraz C., Demaille J., Bensaïd A., Frutos R.;
RT "Analysis of the major antigenic protein 1 multigene family of
RL Ehrlichia ruminantium strain Gardel.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652746; AAV73824.1; -; Genomic DNA.
SQ SEQUENCE 282 AA; 31052 MW; 0CB3C649A691BC90 CRC64;

Query Match 76.7%; Score 1121; DB 2; Length 282;
Best Local Similarity 76.0%; Pred. No. 7e-81;
Matches 215; Conservative 26; Mismatches 38; Indels 4; Gaps 3

Qy      1 MNYKKILVRSALISLMSILPYQSPADPVGSR--NDN-KEGFIYSAKYNPISHERKPSA 57
Db      1 MNYKKILVRSALISLMSFLPYQSPFAEPVSSNIGNENAKEGFIYSAKYNPISIPHRKPSA 60
Qy      58 EETPINGNSLTKKYVGLKKCGDITFKODDFTRVAPGIDFQNNLISGFGSGISGYMDGPRI 117
Db      61 EETPVYKDSPTKKYVGLKKGSIKYSDFTRTDISFQNNNFISGFGSGIGYIMDGPV 120
Qy      118 ELEAYQGFNPKNNTDNDNGEYKHPALSRKDAMEDQYVVLKNDGITFMSLMVNTCY 177
Db      121 EIEAYQGFNPKN-PANETDTSYKYKHYGLSRAEAMADKKYVVLNNGVTFSSLMFNACY 179
Qy      178 DITAGGVFPVPACAGIAGDLITIFKDLNLKPAYQCKIGISVPIPTPEVSFAFIGGYHGV 237
Db      180 DITAGGVFPVPACAGIAGDLISIFDDINLKPAYQCKIGISVPIPTPEISAFIGGYHGV 239
Qy      238 GNKFEKIPVITPVLNDAPQTTASVTLTDVGYFGGIEIGMRFTF 280
Db      240 GNKYNKIPVKLPVTLTDAQOSTASVTLTDAGYFGGELGVRFTF 282

RESULT 10
Q5FGL4 EHRRG
ID Q5FGL4 EHRRG PRELIMINARY; PRT; 304 AA.
AC Q5FGL4
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Map1-related protein.
GN OrderedLocusNames=ERGA_CDS_09150;
OS Ehrlichia ruminantium (strain Gardel).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=302409;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Gardel.
RA Frutos R., Ferraz C., Bensaïd A., Eychenie S., Kandassami Y.,
RA Chantal I., Morgat A., Coissac E., Vachery N., Demaille J., Viari A.,

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QY 178 DITAGVSPVPYACAGIGADLITIPKDLNLKPAYQKGIGISYPIPIPEVSAPFSGYHHGV 237
DB 202 DITAGVSPVPYACAGIGADLISFDDINLKPAYQKGIGISYPIPIPEVSAPFSGYHHGV 261
QY 238 GNKPEKIPVITPVVLNDAPQTTASVTLDVGYFGGEGMRFTF 280
DB 262 GNKNKVPVKLPVTLTDAQSTASVTLDAQYFGGELGVRFTF 304

RESULT 12
QSHA10_EHRRW
ID QSHA10_EHRRW PRELIMINARY; PRT; 282 AA.
AC QSHA10;
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE Putative outer membrane protein MAPI-1.
GN Name=map1-1; OrderedLocusNames=Erum8730;
OS Ehrlichia ruminantium (Strain Welgevonden).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=254945;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15637156; DOI=10.1073/pnas.0406633102;
RA Collins N.E., Liebenberg J., de Villiers E.P., Brayton K.A., Louw E.,
RA Pretorius A., Faber F.E., van Heerden H., Josemans A., van Kleef M.,
RA Steyn H.C., van Strijp M.F., Zweygarth E., Jongejan F., Maillard J.C.,
RA Berthier D., Botha M., Joubert F., Corton C.H., Thomson N.R.,
RA Allsopp M.T., Allsopp B.A.;
RT "The genome of the heartwater agent Ehrlichia ruminantium contains multiple tandem repeats of actively variable copy number.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:838-843 (2005).
DR EMBL; CR767821; CAH58608.1; -; Genomic_DNA.
DR InterPro; IPR011539; RHD.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF01617; Surface_Ag_2; 1.
KW Complete proteome.
SQ SEQUENCE 282 AA; 31100 MW; 1CB2DA256B2CA990 CRC64;

Query Match 76.6%; Score 1120; DB 2; Length 282;
Best Local Similarity 75.6%; Pred. No. 8.4e-81;
Matches 214; Conservative 26; Mismatches 39; Indels 4; Gaps 3;

QY 1 MNYKKILVRSALISLSILPYQSFADPVGSR--NDN-KEGFYISAKNPSISHFRKFS 57
DB 1 MNYKKILVRSALISLSILPYQSFADPVGSR--NDN-KEGFYISAKNPSISHFRKFS 60
QY 58 EETPNTGNSLTKKVFLGKGGDITKDDFTRVAPGIDFQNNLISGFSIGYSMDGPR 117
DB 61 EETPVYKDSPTKKVFLGKGGDITKDDFTRVAPGIDFQNNLISGFSIGYSMDGPR 120
QY 118 ELEAYQQFNPKNTDNDNGEYKHFALSRKDMEDQYVVLKNDGITFMSLMVNTCY 177
DB 121 EIEAYQKFNPKN-PANETDTSYKHYGLSRAETMDKKYVLTNGVTFSSLMFNACY 179
QY 178 DITAGVSPVPYACAGIGADLITIPKDLNLKPAYQKGIGISYPIPIPEVSAPFSGYHHGV 237
DB 180 DITAGVSPVPYACAGIGADLISFDDINLKPAYQKGIGISYPIPIPEVSAPFSGYHHGV 239
QY 238 GNKPEKIPVITPVVLNDAPQTTASVTLDVGYFGGEGMRFTF 280
DB 240 GNKNKVPVKLPVTLTDAQSTASVTLDAQYFGGELGVRFTF 282

RESULT 14
Q3DD4_EHRC
ID Q3DD4_EHRC PRELIMINARY; PRT; 275 AA.
AC Q3DD4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE Outer membrane protein p28.
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=945;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=V2;
RX MEDLINE=21893092; PubMed=11895944;
RX DOI=10.1128/JAI.70.4.1824-1831.2002;
RA Long S.W., Zhang X.F., Qi H., Standaert S., Walker D.H., Yu X.J.;
RT "Antigenic variation of Ehrlichia chaffeensis resulting from differential expression of the 28-kilodalton protein gene family.";

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DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Major antigenic protein 1 like protein (MAP1-1).
OS Ehrlichia ruminantium (Cowdria ruminantium).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=779;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99216274; PubMed=10198207; DOI=10.1006/bbrc.1999.0459;
RA Sulsona C.R., Mahan S.M., Barbet A.F.;
RT "The map1 gene of Cowdria ruminantium is a member of a multigene family containing both conserved and variable genes.";
RL Biochem. Biophys. Res. Commun. 257:300-305 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Welgevonden;
RA van Heerden H., Collins N.E., Brayton K.A., Rademeyer C.,
RA Allsopp B.A.;
RT "Characterization of a major outer membrane protein multigene family in Ehrlichia ruminantium.";
RL Gene 330:159-168 (2004).
DR EMBL; AF125276; AAD26347.1; -; Genomic_DNA.
DR EMBL; AF125275; AAD26345.1; -; Genomic_DNA.
DR EMBL; AY343331; AAR10944.1; -; Genomic_DNA.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 282 AA; 31100 MW; 1CB2DA256B2CA990 CRC64;

Query Match 76.6%; Score 1120; DB 2; Length 282;
Best Local Similarity 75.6%; Pred. No. 8.4e-81;
Matches 214; Conservative 26; Mismatches 39; Indels 4; Gaps 3;

QY 1 MNYKKILVRSALISLSILPYQSFADPVGSR--NDN-KEGFYISAKNPSISHFRKFS 57
DB 1 MNYKKILVRSALISLSILPYQSFADPVGSR--NDN-KEGFYISAKNPSISHFRKFS 60
QY 58 EETPNTGNSLTKKVFLGKGGDITKDDFTRVAPGIDFQNNLISGFSIGYSMDGPR 117
DB 61 EETPVYKDSPTKKVFLGKGGDITKDDFTRVAPGIDFQNNLISGFSIGYSMDGPR 120
QY 118 ELEAYQQFNPKNTDNDNGEYKHFALSRKDMEDQYVVLKNDGITFMSLMVNTCY 177
DB 121 EIEAYQKFNPKN-PANETDTSYKHYGLSRAETMDKKYVLTNGVTFSSLMFNACY 179
QY 178 DITAGVSPVPYACAGIGADLITIPKDLNLKPAYQKGIGISYPIPIPEVSAPFSGYHHGV 237
DB 180 DITAGVSPVPYACAGIGADLISFDDINLKPAYQKGIGISYPIPIPEVSAPFSGYHHGV 239
QY 238 GNKPEKIPVITPVVLNDAPQTTASVTLDVGYFGGEGMRFTF 280
DB 240 GNKNKVPVKLPVTLTDAQSTASVTLDAQYFGGELGVRFTF 282

RESULT 14
Q3DD4_EHRC
ID Q3DD4_EHRC PRELIMINARY; PRT; 275 AA.
AC Q3DD4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE Outer membrane protein p28.
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=945;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=V2;
RX MEDLINE=21893092; PubMed=11895944;
RX DOI=10.1128/JAI.70.4.1824-1831.2002;
RA Long S.W., Zhang X.F., Qi H., Standaert S., Walker D.H., Yu X.J.;
RT "Antigenic variation of Ehrlichia chaffeensis resulting from differential expression of the 28-kilodalton protein gene family.";

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RL	Infect.	Immun.	70:1924-1831(2002).
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RA	STRAIN=V2;		
RA	Yu X.-J., Zhang X.-P., Walker D.H.;		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBDJ databases.		
DR	EMBL; AF393339; AAL12919.1; -- Genomic_DNA.		
DR	InterPro; IPR002566; Surface_Ag_msp4.		
DR	Pfam; PF01617; Surface_Ag_2; 1.		
SQ	SEQUENCE	275 AA; 29374 MW; 2ECCF2F988B2E9D9 CRC64;	
Query Match	45.5%; Score 665.5; DB 2; Length 275;		
Best Local Similarity	49.0%; Pred No. 1.le-44;		
Matches 140; Conservative 43; Mismatches 86; Indels 17; Gaps 5;			
Qy	1 MNYKKILVRSA LISMSILPYQSADPVGSRNDNKEGFYISAKYNPSISHFRKFSAEET	60	
Dd	: : : : : : : :		
Dd	1 MNYKKVFITSA LISLSLPGVSPDPGSGINGN--FYISGYKMPSASHFGVFSAKE-	56	
Qy	61 PINGTNSLTKKVFLKKDGD-----ITKDDDFTRVAPGIDFQNLLISGPSGSIGYMDG	114	
Dd	: : : : : : : :		
Dd	57 -----ERNNTAGVFLGKDWDGSAIPHTQSSPTFTVSYSFKYENNPFLGAFAGIYMDG	112	
Qy	115 PRIELEAAOQFNPKNTDNNDTNGEYYKHFPALSKDAMEDQQVVVLKNDGITMSSLWN	174	
Dd	: : : : : : : :		
Dd	113 PRIELVSYETFDVNQGNN--YKNEAHRYCALRSQTIANDKVKFLKNBGLLDISPLN	170	
Qy	175 TCYDITAEGVSVPYACAGIGADLIITIFKDLNLFAYOGKIGISYPITPEVSFAFIGYYH	234	
Dd	: : : : : : : :		
Dd	171 ACYDVISEGIPFPSVICAGIGTDLVSMFEVTPNKISYQKLGLSYSISPETSVPVGGHF	230	
Qy	235 GVINCKEKPIPVITPVNLNDAPQTTSASVTLDGVFGGEICGMRTTF	280	
Dd	: : : : : : : :		
Dd	231 KVMGNFRDPAIIIPSGSN-LTGHNHPAIVTLDVCHGLEUGGRFAP	275	
RESULT 15			
Q8GGUO_EHRCH			
ID	Q8GGUO_EHRCH PRELIMINARY; PRS; 276 AA.		
AC	Q8GGUO;		
DT	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	28kDa outer membrane protein gene 19.		
OS	Ehrlichia chaffeensis.		
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;		
OX	Anaplasmataceae; Ehrlichia.		
OX	NCBI_TaxId=945;		
RP	[1]		
RP	NUCLEOTIDE SEQUENCE		
RX	MEDLINE=22384137; PubMed=12496165; DOI=10.1128/IAI.71.1.187-195.2003;		
RA	Cheng C., Padcock C.D., Ganta R.R.;		
RT	"Molecular heterogeneity of Ehrlichia chaffeensis isolates determined by sequence analysis of the 28-kilodalton outer membrane protein genes and other regions of the genome.";		
RL	Infect. Immun. 71:187-195(2003).		
DR	EMBL; AF479838; AAC12958.1; -- Genomic_DNA.		
DR	InterPro; IPR002566; Surface_Ag_msp4.		
DR	Pfam; PF01617; Surface_Ag_2; 1.		
SQ	SEQUENCE	276 AA; 30045 MW; 8E3C9719D3C67A64 CRC64;	
Query Match	44.8%; Score 655; DB 2; Length 276;		
Best Local Similarity	48.8%; Pred No. 7.7e-44;		
Matches 140; Conservative 43; Mismatches 86; Indels 18; Gaps 6;			
Qy	1 MNYKKILVRSA LISMSILPYQSADPVGSRNDNKEGFYISAKYNPSISHFRKFSAEET	60	
Dd	: : : : : : : :		
Dd	1 MNYKKVFITSA LISLSLPGVSPDPGSGINGN--FYISGYKMPSASHFGVFSAKE-	56	
Qy	61 PINGTNSLTKKVFLKKDGD-----ITKDDDFTRVAPGIDFQNLLISGPSGSIGYMDG	114	
Dd	: : : : : : : :		
Dd	57 -----ERNNTAGVFLGKDWDGSAIPHTQSSPTFTVSYSFKYENNPFLGAFAGIYMDG	112	

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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:47:54 ; Search time 2.88889 Seconds
(without alignments)
91.208 Million cell updates/sec

Title: US-10-680-349-42_COPY_61_86
Perfect score: 136
Sequence: 1 PINGNSLTKVFGKKGDDITKDD 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70609 seqs, 10134256 residues

Total number of hits satisfying chosen parameters: 70609

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
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3: /cgn2_6/prodata/1/pubpa/US07_NEW_PUB.pep.*
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5: /cgn2_6/prodata/1/pubpa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/1/pubpa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	36.8	302	6	US-10-467-657-80
2	50	36.8	302	6	US-10-467-657-4818
3	49	36.0	1992	7	US-11-013-759-3
4	49	36.0	1992	7	US-11-013-759-13
5	49	36.0	2047	7	US-11-013-759-4
6	49	36.0	2047	7	US-11-013-759-7
7	48.5	35.7	476	7	US-11-069-642-19
8	48.5	35.7	585	6	US-10-510-386-20
9	48.5	35.7	594	6	US-10-510-386-38
10	47.5	34.9	295	6	US-10-201-525-13
11	45	33.1	138	6	US-10-793-626-2878
12	45	33.1	817	6	US-10-793-626-2948
13	44	32.4	421	6	US-10-467-657-790
14	44	32.4	433	6	US-10-793-626-1332
15	44	32.4	783	7	US-11-192-219-7
16	42	30.9	416	6	US-10-641-678-73
17	42	30.9	556	6	US-10-467-657-498
18	42	30.9	1386	6	US-10-517-939-284
19	41	30.1	129	7	US-11-125-402-24
20	41	30.1	129	7	US-11-125-402-33
21	41	30.1	130	7	US-11-125-402-29
22	41	30.1	1431	7	US-11-128-059-2
23	41	30.1	3712	7	US-11-019-711-48
24	41	30.1	3712	7	US-11-019-711-51
25	40.5	29.8	364	6	US-10-984-376-5

26	40.5	29.8	364	6	US-10-984-376-6	Sequence 6, Appli
27	40.5	29.8	437	6	US-10-525-710-18	Sequence 18, Appl
28	40.5	29.4	115	6	US-10-793-626-1560	Sequence 1560, Ap
29	40.5	29.4	133	7	US-11-082-389-438	Sequence 428, App
30	40.5	29.4	295	6	US-10-467-657-8344	Sequence 8344, Ap
31	40.5	29.4	347	6	US-10-467-657-2962	Sequence 2962, Ap
32	40.5	29.4	697	7	US-11-082-389-362	Sequence 338, App
33	39	28.7	156	7	US-11-082-389-338	Sequence 1, Appli
34	39	28.7	229	6	US-10-656-894-1	Sequence 2, Appli
35	39	28.7	229	6	US-10-656-894-2	Sequence 3, Appli
36	39	28.7	229	6	US-10-656-894-3	Sequence 4, Appli
37	39	28.7	229	6	US-10-656-894-4	Sequence 356, App
38	39	28.7	309	6	US-10-793-626-356	Sequence 1278, Ap
39	39	28.7	341	6	US-10-793-626-1278	Sequence 14, Appl
40	39	28.7	421	7	US-11-214-199-14	Sequence 184, App
41	39	28.7	577	7	US-11-074-176-184	Sequence 62, Appl
42	39	28.7	597	7	US-11-074-176-62	Sequence 4290, Ap
43	39	28.7	924	6	US-10-467-657-4290	Sequence 4, Appli
44	39	28.7	2376	7	US-11-096-051-4	Sequence 2, Appli
45	39	28.7	2715	7	US-11-096-051-2	

ALIGNMENTS

RESULT 1
US-10-467-657-80
; Sequence 80, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwinn9, version 1.04
; SEQ ID NO 80
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-80

Query Match 36.8%; Score 50; DB 6; Length 302;
Best Local Similarity 57.9%; Pred. No. 1.9;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 GTNSLTKVFGKKGDDIT 22
||| ||| ||| ||| :||
Db 27 GTIKTKATFHLKDDTSLT 45

RESULT 2
US-10-467-657-4818
; Sequence 4818, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8

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; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4818
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4818

Query Match      36.8%; Score 50; DB 6; Length 302;
Best Local Similarity 57.9%; Pred. No. 1.9;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 GTNSLTKKVFGKKGDDIT 22
Db 27 GTIKLTAKTHLKKQTSLT 45

RESULT 3
US-11-013-759-3
; Sequence 3, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN OF MORAXELLA
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1992
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-3

Query Match      36.0%; Score 49; DB 7; Length 1992;
Best Local Similarity 38.1%; Pred. No. 26;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 GTNSLTKKVFGKKGDDITK 24
Db 430 GTTRITRDKIGFARDGDVDEK 450

RESULT 4
US-11-013-759-13
; Sequence 13, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN OF MORAXELLA
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1992
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
,

US-11-013-759-13
Query Match      36.0%; Score 49; DB 7; Length 1992;
Best Local Similarity 38.1%; Pred. No. 26;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 GTNSLTKKVFGKKGDDITK 24
Db 430 GTTRITRDKIGFARDGDVDEK 450

RESULT 5
US-11-013-759-4
; Sequence 4, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN OF MORAXELLA
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2047
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-4

Query Match      36.0%; Score 49; DB 7; Length 2047;
Best Local Similarity 38.1%; Pred. No. 27;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 GTNSLTKKVFGKKGDDITK 24
Db 485 GTTRITRDKIGFARDGDVDEK 505

RESULT 6
US-11-013-759-7
; Sequence 7, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN OF MORAXELLA
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2047
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-7

Query Match      36.0%; Score 49; DB 7; Length 2047;
Best Local Similarity 38.1%; Pred. No. 27;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 GTNSLTKKVFGKKGDDITK 24
Db 485 GTTRITRDKIGFARDGDVDEK 505
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Db      485 GTTTRTDKIGFARDGVDDEK 505
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RESULT 7
US-11-069-642-19
; Sequence 19, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Pyrococcus horikoshii OT3
US-11-069-642-19
Query Match      35.7%; Score 48.5; DB 7; Length 476;
Best Local Similarity 57.9%; Pred. No. 5.4;
Matches 11; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 11 KVP---GLKKGDDITKKDD 26
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Db 96 KVFTSGLKEAGEITEKDE 114
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RESULT 8
US-10-510-386-20
; Sequence 20, Application US/10510386
; Publication No. US2005024922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-20
Query Match      35.7%; Score 48.5; DB 6; Length 585;
Best Local Similarity 59.1%; Pred. No. 7;
Matches 13; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 2 INGTNSLTKKVFG-LKKDGDIT 22
|:| | | | | | | | | | | | | |
Db 432 ISGTGKLTKKGTGALKLEGDNT 453
|:| | | | | | | | | | | | | |

RESULT 9
US-10-510-386-38
; Sequence 38, Application US/10510386
; Publication No. US2005024922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-38
Query Match      35.7%; Score 48.5; DB 6; Length 594;
Best Local Similarity 59.1%; Pred. No. 7.1;
Matches 13; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 2 INGTNSLTKKVFG-LKKDGDIT 22
|:| | | | | | | | | | | | | |
Db 437 ISGTGKLTKKGTGALKLEGDNT 458
|:| | | | | | | | | | | | | |

RESULT 10
US-10-201-525-13
; Sequence 13, Application US/10201525
; Publication No. US20060009631A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 5827.005
; CURRENT APPLICATION NUMBER: US/10/201,525
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/785,343
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/16750
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-201-525-13
Query Match      34.9%; Score 47.5; DB 6; Length 295;
Best Local Similarity 37.0%; Pred. No. 4.3;
Matches 10; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 PINGTNSLTKKVFG-LKKDGDITK-KDD 26
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Db 47 PKSGTTWISEVYVMIYKGDVEKCKED 73
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RESULT 11
US-10-793-626-2878
; Sequence 2878, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
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; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2878
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of A
; OTHER INFORMATION: amino acid sequen
US-10-793-626-2878

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Query Match 33.1%; Score 45; DB 6; Length 138;
Best Local Similarity 53.3%; Pred. No. 4;
Matches 8; Conservative 2; Mismatches 5; Indels

Qy 4 GTNSLTKKVFGLKGD 18
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Db 28 GTNDLTOLTEGFSRD 42

RESULT 12

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US-10-793-626-2948
; Sequence 2948, Application US/10793626
; Publication No. US2005025478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P034800S
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2948
; LENGTH: 817
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (817)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2948

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Query Match 33.1%; Score 45; DB 6; Length 817;
Best Local Similarity 53.3%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 5; Indels

Qy 4 GTNSLTKKVFGLKKD 18
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Db 751 GTNDLTQLTFGFSRD 765

RESULT 13

US-10-467-657-790
; Sequence 790, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8

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; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 790
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-790

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Query Match 32.4%; Score 44; DB 6; Length 421;
Best Local Similarity 36.0%; Pred. No. 22;
Matches 9: Conservative 4; Mismatches 12; Indels

Qy 1 PINGNSLTKKVFLGKKGDIKKD 25
|::| : | :||| |
Db 301 PMDGKKEADQPDFAKDPEGDIKKD 325

RESULT 14

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US-10-793-626-1332
; Sequence 1332, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1332
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1332

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Query Match	32.4%;	Score 44;	DB 6;	Length 433;
Best Local Similarity	52.2%;	Pred. No. 23;		
Matches 12: Conservative	2;	Mismatches	7;	Indels
			2;	Gaps 1;

Qy 3 NGTNSLTKKVFGLKKDGDITKKD 25
140 NGVN--IKAVNGSGKNGRITKED 160
Db

RESULT 15

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US-11-192-219-7
; Sequence 7, Application US/11192219
; Publication No. US20050272656A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Matthews, William
;
; TITLE OF INVENTION: USES FOR WSX LIGANDS
;
; NUMBER OF SEQUENCES: 47
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Genentech, Inc.
;
; STREET: 460 Point San Bruno Blvd
;
; CITY: South San Francisco
;
; STATE: California
;
; COUNTRY: USA
;
; ZIP: 94080
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: WinPatIn (Genentech)
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/11/192,219
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; FILING DATE: 27-Jul-2005
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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,197
; FILING DATE: 20-Jun-1996
; APPLICATION NUMBER: 08/585005
; FILING DATE: 08-Jan-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: P-40,378
; REFERENCE/DOCKET NUMBER: P0986P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-11-192-219-7

Query Match      32.4%; Score 44; DB 7; Length 783;
Best Local Similarity 61.5%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      13 FGLKKDGDITKKD 25
Db      643 FWRKMDGDVTKKE 655
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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:46:59 ; Search time 14.3595 Seconds
(without alignments)
756.543 Million cell updates/sec

Title: US-10-680-349-42_COPY_61_86
Perfect score: 136
Sequence: 1 PINGTNSLTKKVFLKDDITKKDD 26

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Total number of hits satisfying chosen parameters: 1867569

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Post-processing: Minimum Match 0%
Maximum Match 100%
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	280	3	US-09-811-007-42
2	136	100.0	280	4	US-10-062-624-42
3	136	100.0	280	4	US-10-059-964-48
4	136	100.0	280	4	US-10-062-051-42
5	136	100.0	280	4	US-10-062-920-42
6	136	100.0	280	4	US-10-314-639-48
7	136	100.0	280	4	US-10-680-349-42
8	136	100.0	280	5	US-10-731-554-42
9	136	100.0	280	5	US-10-901-714-48
10	136	100.0	280	5	US-10-901-774-48
11	97	71.3	283	3	US-09-846-808-14
12	97	71.3	283	3	US-09-811-007-10
13	97	71.3	283	4	US-10-062-624-10
14	97	71.3	283	4	US-10-059-964-4
15	97	71.3	283	4	US-10-062-051-10
16	97	71.3	283	4	US-10-284-986-14
17	97	71.3	283	4	US-10-062-920-10
18	97	71.3	283	4	US-10-314-639-4
19	97	71.3	283	4	US-10-369-293-14
20	97	71.3	283	4	US-10-285-042-14
21	97	71.3	283	4	US-10-680-349-10
22	97	71.3	283	5	US-10-731-554-10
23	97	71.3	283	5	US-10-901-714-4
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25	54.5	40.1	70	4	US-10-424-599-158286
26	53	39.0	361	4	US-10-424-599-204976
27	52.5	38.6	339	4	US-10-369-493-4102

28	52	38.2	377	4	US-10-282-122A-57079	Sequence 57079, A
29	52	38.2	481	4	US-10-282-122A-48632	Sequence 48632, A
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32	50.5	37.1	873	4	US-10-369-493-11332	Sequence 11332, A
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34	50	36.8	283	5	US-10-901-714-69	Sequence 69, Appl
35	50	36.8	283	5	US-10-901-774-69	Sequence 69, Appl
36	50	36.8	284	3	US-09-811-007-15	Sequence 15, Appl
37	50	36.8	284	4	US-10-062-624-15	Sequence 15, Appl
38	50	36.8	284	4	US-10-062-051-15	Sequence 15, Appl
39	50	36.8	284	4	US-10-062-920-15	Sequence 15, Appl
40	50	36.8	284	4	US-10-680-349-15	Sequence 15, Appl
41	50	36.8	284	5	US-10-731-554-15	Sequence 15, Appl
42	49.5	36.4	205	4	US-10-767-701-41494	Sequence 41494, A
43	49.5	36.4	346	5	US-10-771-620-6	Sequence 6, Appl
44	49.5	36.4	521	3	US-09-820-843A-93	Sequence 93, Appl
45	49.5	36.4	529	5	US-10-771-620-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-811-007-42
; Sequence 42, Application US/09811007
; Publication No. US20030185849A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/811,007
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-09-811-007-42

Query Match 100.0%; Score 136; DB 3; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFLKDDITKKDD 26
DB 61 PINGTNSLTKKVFLKDDITKKDD 86

RESULT 2
US-10-062-624-42
; Sequence 42, Application US/10062624
; Publication No. US20020115840A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2/D1
; CURRENT APPLICATION NUMBER: US/10/062,624
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42

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; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-10-062-624-42

Query Match      100.0%; Score 136; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 PINGTNSLTKKVFGGLKKDGDITKKDD 86

RESULT 3
US-10-059-964-48
; Sequence 48, Application US/10059964
; Publication No. US20020120115A1
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohasi, No. US20020120115A1io
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/10/059,964
; CURRENT FILING DATE: 2002-01-28
; EARLIER APPLICATION NUMBER: 09/314,701
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-10-059-964-48

Query Match      100.0%; Score 136; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 PINGTNSLTKKVFGGLKKDGDITKKDD 86

RESULT 4
US-10-062-051-42
; Sequence 42, Application US/10062051
; Publication No. US20030073095A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/10/062,051
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/660,587
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US/09/660,587
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
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US-10-062-051-42
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US-10-062-920-42
; Sequence 42, Application US/10062920
; Publication No. US20030096250A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/10/062,920
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/660,587
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
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; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
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; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-10-062-920-42

Query Match      100.0%; Score 136; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-10-314-639-48
; Sequence 48, Application US/10314639
; Publication No. US20030103991A1
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohasi, No. US20030103991A1io
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/10/314,639
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/314,701
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-10-314-639-48

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Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
US-10-314-639-48
; Sequence 48, Application US/10314639
; Publication No. US20030103991A1
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohasi, No. US20030103991A1io
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/10/314,639
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/314,701
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-10-314-639-48

Query Match      100.0%; Score 136; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7

US-10-680-349-42
; Sequence 42, Application US/10680349
; Publication No. US20040198951A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2/D1
; CURRENT APPLICATION NUMBER: US/10/680,349
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US/10/062,624
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
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; TYPE: PRT
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US-10-680-349-42

Query Match 100.0%; Score 136; DB 4; Length 280;
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-731-554-42
; Sequence 42, Application US/10731554
; Publication No. US20040247616A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/10/731,554
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: US/09/811,007
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-10-731-554-42

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Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKKGDIKKDD 26
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Db 61 PINGTNSLTKKVFGKKGDIKKDD 86

RESULT 9

US-10-731-554-42

US-10-901-714-48
; Sequence 48, Application US/10901714
; Publication No. US20040265333A1
; GENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
; APPLICANT: OHASHI, NORIO
; TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRlichia CANIS AND EHRlichia
; FILE REFERENCE: 22727-04109
; CURRENT APPLICATION NUMBER: US/10/901,714
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 09/314,701
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/100,843
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-10-901-714-48

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 PINGTNSLTKKVFGKKGDIKKDD 86

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; Sequence 48, Application US/10901774
; Publication No. US20040265334A1
; GENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
; APPLICANT: OHASHI, NORIO
; TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRlichia CANIS AND EHRlichia
; FILE REFERENCE: 22727-04109
; CURRENT APPLICATION NUMBER: US/10/901,774
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 09/314,701
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/100,843
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-10-901-774-48

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Db 61 PINGTNSLTKKVFGKKGDIKKDD 86

RESULT 11

US-09-846-808-14
; Sequence 14, Application US/09846808
; Patent No. US20020064531A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: Yu, Xu-Jie
; TITLE OF INVENTION: Ehrlichia chaffeensis 28 kDa Outer Membrane

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; TITLE OF INVENTION: Protein Multigene Family
; FILE REFERENCE: D6311
; CURRENT APPLICATION NUMBER: US/09/846,808
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/201,035
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 53
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; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: P28-14 Outer Membrane Protein of
; OTHER INFORMATION: Ehrlichia chaffeensis
US-09-846-808-14

Query Match          71.3%; Score 97; DB 3; Length 283;
Best Local Similarity 78.3%; Pred. No. 7.5e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 64 PINGNTSITKKVFLGKKGDIYK 86

RESULT 12
US-09-811-007-10
; Sequence 10, Application US/09811007
; Publication No. US20030185849A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/811,007
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 10
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
US-09-811-007-10

Query Match          71.3%; Score 97; DB 3; Length 283;
Best Local Similarity 78.3%; Pred. No. 7.5e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 64 PINGNTSITKKVFLGKKGDIYK 86

RESULT 13
US-10-062-624-10
; Sequence 10, Application US/10062624
; Publication No. US20020115840A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2/D1
; CURRENT APPLICATION NUMBER: US/10/062,624
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B

; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 10
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
US-10-062-624-10

Query Match          71.3%; Score 97; DB 4; Length 283;
Best Local Similarity 78.3%; Pred. No. 7.5e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGNSLTKKVFLGKKGDIYK 23
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Db 64 PINGNTSITKKVFLGKKGDIYK 86

RESULT 14
US-10-059-964-4
; Sequence 4, Application US/10059964
; Publication No. US20020120115A1
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohasi, No. US20020120115A1io
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/10/059,964
; CURRENT FILING DATE: 2002-01-28
; EARLIER APPLICATION NUMBER: 09/314,701
; EARLIER FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-10-059-964-4

Query Match          71.3%; Score 97; DB 4; Length 283;
Best Local Similarity 78.3%; Pred. No. 7.5e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 64 PINGNTSITKKVFLGKKGDIYK 86

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US-10-062-051-10
; Sequence 10, Application US/10062051
; Publication No. US20030073095A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/10/062,051
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/660,587
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 10
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
US-10-062-051-10
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US-10-062-051-10

Query Match 71.3%; Score 97; DB 4; Length 283;
Best Local Similarity 78.3%; Pred. No. 7.5e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	136	100.0	280	2	US-09-314-701-48
3	136	100.0	280	2	US-09-811-007A-42
4	136	100.0	280	2	US-10-314-639-48
5	136	100.0	280	2	US-10-059-964A-48
6	97	71.3	283	2	US-09-660-587-10
7	97	71.3	283	2	US-09-261-358A-10
8	97	71.3	283	2	US-09-201-458-6
9	97	71.3	283	2	US-09-314-701-4
10	97	71.3	283	2	US-09-811-007A-10
11	97	71.3	283	2	US-10-314-639-4
12	97	71.3	283	2	US-10-059-964A-4
13	52	38.2	378	2	US-09-134-000C-5909
14	50	36.8	283	2	US-10-059-964A-69
15	50	36.8	284	2	US-09-660-587-15
16	50	36.8	284	2	US-09-261-358A-15
17	50	36.8	284	2	US-09-201-458-11
18	50	36.8	284	2	US-09-811-007A-15
19	49	36.0	629	2	US-10-081-923-6
20	49	36.0	1833	2	US-08-621-944A-4
21	49	36.0	1833	2	US-08-945-567D-4
22	49	36.0	1992	2	US-08-621-944A-3
23	49	36.0	1992	2	US-08-945-567D-3
24	49	36.0	2048	2	US-09-268-347-48
25	48.5	35.7	416	1	US-08-464-523B-33
26	48.5	35.7	476	2	US-09-800-170-19
27	48	35.3	226	2	US-09-071-035-120

28	48	35.3	226	2	US-10-206-576-120	Sequence 120, App
29	48	35.3	252	2	US-09-071-035-118	Sequence 118, App
30	48	35.3	252	2	US-10-206-576-118	Sequence 118, App
31	48	35.3	293	2	US-09-660-587-40	Sequence 40, Appl
32	48	35.3	293	2	US-09-314-701-44	Sequence 44, Appl
33	48	35.3	293	2	US-09-811-007A-40	Sequence 40, Appl
34	48	35.3	293	2	US-10-314-639-44	Sequence 44, Appl
35	48	35.3	293	2	US-10-059-964A-44	Sequence 44, Appl
36	48	35.3	300	2	US-09-314-701-50	Sequence 50, Appl
37	48	35.3	300	2	US-10-314-639-50	Sequence 50, Appl
38	48	35.3	300	2	US-10-059-964A-50	Sequence 50, Appl
39	47.5	34.9	295	2	US-09-150-133-13	Sequence 13, Appl
40	47.5	34.9	295	2	US-09-150-141-13	Sequence 13, Appl
41	47.5	34.9	295	2	US-09-374-493-13	Sequence 13, Appl
42	47.5	34.9	295	2	US-09-374-824-13	Sequence 13, Appl
43	47.5	34.9	295	2	US-09-374-492-13	Sequence 13, Appl
44	47.5	34.9	295	2	US-09-785-343-13	Sequence 13, Appl
45	47.5	34.9	295	2	US-10-411-976-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-660-587-42
; Sequence 42, Application US/09660587
; Patent No. 6392023
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/660,587
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-09-660-587-42

Query Match 100.0%; Score 136; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 5.6e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PINGNSLTKKVFGKKGDDITKKDD 26
|||||
Db 61 PINGNSLTKKVFGKKGDDITKKDD 86

RESULT 2
US-09-314-701-48
; Sequence 48, Application US/09314701
; Patent No. 6544517
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohashi, No. 6544517iO
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; TITLE OF INVENTION: Chaffensis
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/09/314,701
; CURRENT FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT

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; ORGANISM: Ehrlichia canis
US-09-314-701-48

Query Match      100.0%; Score 136; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 5.6e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKKGDDITKKDD 26
Db 61 PINGTNSLTKKVFGKKGDDITKKDD 86
|||||

RESULT 3
US-09-811-007A-42
; Sequence 42, Application US/09811007A
; Patent No. 6660269
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/811,007A
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 42
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-09-811-007A-42

Query Match      100.0%; Score 136; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 5.6e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKKGDDITKKDD 26
Db 61 PINGTNSLTKKVFGKKGDDITKKDD 86
|||||

RESULT 4
US-10-314-639-48
; Sequence 48, Application US/10314639
; Patent No. 6893640
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Chasi, No. 6893640io
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; TITLE OF INVENTION: Chaffeensis
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/10/314,639
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/314,701
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-10-314-639-48

Query Match      100.0%; Score 136; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 5.6e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKKGDDITKKDD 26
Db 61 PINGTNSLTKKVFGKKGDDITKKDD 86
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RESULT 5
US-10-059-964A-48
; Sequence 48, Application US/10059964A
; Patent No. 6923963
; GENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
; APPLICANT: OHASHI, NORIO
; TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRlichia CANIS AND EHRlichia
; TITLE OF INVENTION: CHAPPEENSIS
; FILE REFERENCE: 22727-04109
; CURRENT APPLICATION NUMBER: US/10/059,964A
; CURRENT FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: 09/314,701
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/100,843
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 48
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-10-059-964A-48

Query Match      100.0%; Score 136; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 5.6e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKKGDDITKKDD 26
Db 61 PINGTNSLTKKVFGKKGDDITKKDD 86
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RESULT 6
US-09-660-587-10
; Sequence 10, Application US/09660587
; Patent No. 6392023
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/660,587
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 10
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
US-09-660-587-10

Query Match      71.3%; Score 97; DB 2; Length 283;
Best Local Similarity 78.3%; Pred. No. 2.8e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKKGDDITK 23
Db 64 PINGTNSITKKVFGKKGDDIAQ 86
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RESULT 7
US-09-261-358A-10
; Sequence 10, Application US/09261358A
; Patent No. 6403780
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; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP
; CURRENT APPLICATION NUMBER: US/09/261,358A
; CURRENT FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 09/201,458
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 10
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
US-09-261-358A-10

Query Match      71.3%; Score 97; DB 2; Length 283;
Best Local Similarity 78.3%; Pred. No. 2.8e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGGLKKGDIK 23
Db 64 PINGNTSITKKVFGGLKKGDIQA 86

RESULT 8
US-09-201-458-6
; Sequence 6, Application US/09201458A
; Patent No. 6458942
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: 28-kDa Immunoreactive Protein Gene of Ehrlichia
; FILE OF INVENTION: canis and Uses Thereof
; FILE REFERENCE: D6152
; CURRENT APPLICATION NUMBER: US/09/201,458A
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 6
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
US-09-201-458-6

Query Match      71.3%; Score 97; DB 2; Length 283;
Best Local Similarity 78.3%; Pred. No. 2.8e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGGLKKGDIK 23
Db 64 PINGNTSITKKVFGGLKKGDIQA 86

RESULT 9
US-09-314-701-4
; Sequence 4, Application US/09314701
; Patent No. 6544517
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohasi, No. 6544517io
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; FILE OF INVENTION: Chaffeensis
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/09/314,701
; CURRENT FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66

QY 1 PINGTNSLTKKVFGGLKKGDIK 23
Db 64 PINGNTSITKKVFGGLKKGDIQA 86

RESULT 10
US-09-811-007A-10
; Sequence 10, Application US/09811007A
; Patent No. 6660269
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/811,007A
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/660,587
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 10
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
US-09-811-007A-10

Query Match      71.3%; Score 97; DB 2; Length 283;
Best Local Similarity 78.3%; Pred. No. 2.8e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGGLKKGDIK 23
Db 64 PINGNTSITKKVFGGLKKGDIQA 86

RESULT 11
US-10-314-639-4
; Sequence 4, Application US/10314639
; Patent No. 6893640
; GENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
; APPLICANT: Ohasi, No. 6893640io
; TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
; FILE OF INVENTION: Chaffeensis
; FILE REFERENCE: 22727/04021
; CURRENT APPLICATION NUMBER: US/10/314,639
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/314,701
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-10-314-639-4

Query Match      71.3%; Score 97; DB 2; Length 283;
Best Local Similarity 78.3%; Pred. No. 2.8e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTQKVFGLKKGGDITK 23
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Db 64 PINGNTSITKVFGLKKGGDIAQ 86

RESULT 12

US-10-059-964A-4
; Sequence 4, Application US/10059964A
; Patent No. 6923963
; GENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
; APPLICANT: OHASHI, NORIO
; TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRlichia CANIS AND EHRlichia
; FILE REFERENCE: 22727-04109
; CURRENT APPLICATION NUMBER: US/10/059,964A
; PRIOR FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: 09/314,701
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/100,843
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-10-059-964A-4

Query Match 71.3%; Score 97; DB 2; Length 283;

Best Local Similarity 78.3%; Pred. No. 2.8e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTQKVFGLKKGGDITK 23
||| | : ||| | ||| | :
Db 64 PINGNTSITKVFGLKKGGDIAQ 86

RESULT 13

US-09-134-000C-5909
; Sequence 5909, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5909
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5909

Query Match 38.2%; Score 52; DB 2; Length 378;

Best Local Similarity 39.1%; Pred. No. 14;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 3 NGTNSLTQKVFGLKKGGDITK 25
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Db 280 NGTNSITSLPKYKENGVEVLND 302

RESULT 14

US-10-059-964A-69
; Sequence 69, Application US/10059964A

; Patent No. 6923963
; GENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
; APPLICANT: OHASHI, NORIO
; TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRlichia CANIS AND EHRlichia
; FILE REFERENCE: 22727-04109
; CURRENT APPLICATION NUMBER: US/10/059,964A
; PRIOR FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: 09/314,701
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/100,843
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 69
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Cowdria ruminantium
US-10-059-964A-69

Query Match 36.8%; Score 50; DB 2; Length 283;

Best Local Similarity 73.3%; Pred. No. 20;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 TKKVFGGLKKGGDITK 23
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Db 63 TKAVFGLKKDWDGVR 77

RESULT 15

US-09-660-587-15
; Sequence 15, Application US/09660587
; Patent No. 6392023
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CIP2
; CURRENT APPLICATION NUMBER: US/09/660,587
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 15
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Cowdria ruminantium
; FEATURE:
; OTHER INFORMATION: amino acid sequence of C. ruminantium MAP-1
US-09-660-587-15

Query Match 36.8%; Score 50; DB 2; Length 284;

Best Local Similarity 73.3%; Pred. No. 20;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 TKKVFGGLKKGGDITK 23
||| | : ||| | ||| | :
Db 63 TKAVFGLKKDWDGVR 77

Search completed: January 24, 2006, 11:49:00
Job time : 5.26797 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:35:23 ; Search time 19.5425 Seconds
(without alignments)
938.659 Million cell updates/sec

Title: US-10-680-349-42_COPY_61_86
Perfect score: 136
Sequence: 1 PINGTNSLTKKVFLKKDGDITKKD

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10
                  Listing first 45

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2: uniprot_trembl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	136	100.0	280	2	Q84HUL_EHRCA	Q84hul ehrlichia c
2	136	100.0	280	2	Q8F476_EHRCA	Q8f476 ehrlichia c
3	101	74.3	283	2	Q8G8D6_EHRCH	Q8g8d6 ehrlichia c
4	101	74.3	283	2	Q8G8U4_EHRCH	Q8g8u4 ehrlichia c
5	98	72.1	283	2	Q8G8I2_EHRCH	Q8g8i2 ehrlichia c
6	97	71.3	283	2	Q8S358_EHRCH	Q8s358 ehrlichia c
7	90	66.2	282	2	Q5W5Y1_EHRRU	Q5w5y1 ehrlichia r
8	86	63.2	282	2	Q9R443_EHRUR	Q9r443 ehrlichia r
9	86	63.2	282	2	Q4LOC0_EHRRU	Q4loc0 ehrlichia r
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14	86	47.1	238	2	Q8A3S3_BACTN	Q8a3s3 bacteroides
15	57	41.9	266	2	Q7R7D4_PLAYO	Q7r7d4 plasmodium
16	57	41.9	266	2	Q7RER7_PLAYO	Q7rer7 plasmodium
17	57	41.9	268	2	Q7RA08_PLAYO	Q7ra08 plasmodium
18	55.5	40.8	481	2	Q5NHN7_FRATT	Q5nhn7 francisella
19	55	40.4	92	2	Q9B3B2_RHIL0	Q9b3b2 rhizobium l
20	54	39.7	1333	2	Q54KL3_DICD1	Q54kl3 dictyosteli
21	53.5	39.3	2515	2	Q77365_PLAYF	Q77365 plasmodium
22	53	39.0	266	2	Q7REB5_PLAYO	Q7reb5 plasmodium
23	53	39.0	426	1	GLYA_TTHEO	Q97cq5 thermoplasma
24	53	39.0	800	2	Q6BNK2_DESHA	Q6bnk2 debaryomyce
25	53	39.0	1730	2	Q7RDQ0_PLAYO	Q7rdq0 plasmodium
26	52.5	38.6	334	2	Q7S7U0_NEUCR	Q7s7u0 neurospora
27	52	38.2	377	2	Q8KU85_ENTPA	Q8ku85 enterococcu
28	52	38.2	481	2	Q5L9U4_BACFN	Q5l9u4 bacteroides
29	52	38.2	481	2	Q6Q408_BACFN	Q6q408 bacteroides
30	52	38.2	912	2	Q519D8_BACFN	Q519d8 bacteroides
31	52	38.2	912	2	Q64PM2_BACFN	Q64pm2 bacteroides

RESULT 1

Q84HU1_EHRCA Q84HU1_EHRCA PRELIMINARY; PRT; 280 AA.
ID Q84HU1_EHRCA PRELIMINARY; PRT; 280 AA.
AC Q84HU1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major outer membrane protein.
GN Name=p30-10;
OS Ehrlichia canis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_Taxid=944;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT STRAIN=Hawaii;
RX MEDLINE=22461952; PubMed=12574308; DOI=10.1128/JCM.41.2.886-888.2003;
RA Pelek S., Greene R., Rikihisa Y.;
RT "Transcriptional Analysis of p30 Major Outer Membrane Protein Genes of
RT Ehrlichia canis in Naturally Infected Ticks and Sequence Analysis of
RT p30-10 of E. canis from Diverse Geographic Regions.";
RL J. Clin. Microbiol. 41:886-888(2003).
DR EMBL; AF528513; AA041110.1; -; Genomic_DNA.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 280 AA; 30990 MW; D1BB28B14F5BDCA2 CRC64;

Query Match	100.0%;	Score 136;	DB 2;	Length 280;
Best Local Similarity	100.0%;	Pred. No. 1.7e-11;		
Matches 26;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

0v 1 PINGTNSLTKKVFGCLKDGDITKKDD 26

61 PINGTNSLTKKVFGCLKKGDTKKDD 86

RESULT 2

Q9F476_EHRCA
ID Q9F476_EHRCA PRELIMINARY; PRT; 280 AA.
AC Q9F476;
AD 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE P28-2 (Major outer membrane protein p30-10).
GN Name=p28-2; Synonyms=p30-10;
OS Ehrlichia canis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=944;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Jake;
RX MEDLINE=992442757; PubMed=10225842;
RA McBride J.W., Yu, Xj, Walker D.H.;

ALIGNMENTS

32	52	38.2	1218	2	Q4P674	USTMA	Q4p674	ustilago ma
33	51.5	37.9	279	2	Q6NW18	BRARE	Q6nw18	brachydanio
34	51.5	37.9	551	2	Q6I637	PUAF7	Q6i637	plasmidium
35	51.5	37.9	562	2	Q6C527	YARLI	Q6c527	yarrowia li
36	51	37.5	321	2	Q6CFV8	YARLI	Q6cfv8	yarrowia li
37	51	37.5	345	2	Q93FL9	9NTR	Q93fl9	citrobacter
38	51	37.5	530	2	Q5KW58	GBOKA	Q5kw58	geobacillus
39	51	37.5	559	2	Q3FR54	ARATH	Q3fr54	arabidopsis
40	51	37.5	948	2	Q84N32	SORBI	Q84n32	sorghum bic
41	51	37.5	1373	2	Q7QR53	PLAJO	Q7qr53	plasmidium
42	51	37.5	1793	2	Q8EWW0	MYCPE	Q8eww0	mycoplasma
43	50.5	37.1	268	2	Q7YTF3	CRYP	Q7ytf3	cryptospori
44	50.5	37.1	281	2	Q4QWR0	CRYP	Q4qwr0	cryptospori
45	50.5	37.1	282	2	Q4QWR0	CRYP	Q4qwr0	cryptospori

RT "Molecular cloning of the gene for a conserved major immunoreactive
RT 28-kilodalton protein of *Ehrlichia canis*: a potential serodiagnostic
RT antigen.";
RL Clin. Diagn. Lab. Immunol. 6:392-399(1999).

RP [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JAKE.
 RC
 RX MEDLINE=20432107; PubMed=10974556; DOI=10.1016/S0378-1119(00)00256-0;
 RX
 RA McBride J.W., Yu X.J., Walker D.H.;
 RT "A conserved, transcriptionally active p28 multigene locus of
 RT *Ehrlichia canis*."
 RL Gene 254:245-252(2000).

[3]
RN
RP
RC NUCLEOTIDE SEQUENCE.
RX STRAIN=Oklahoma;
RY MEDLINE=98371112; PubMed=9705412;
RA Ohashi N., Unver A., Zhi N., Rikihisa Y.;
RT "Cloning and characterization of multigenes encoding the
RT immunodominant 30-kilodalton major outer membrane proteins of
RT *Escherichia canis* and application of the recombinant protein for
RT serodiagnosis";
RL J. Clin. Microbiol. 36:2671-2680(1998).

[4]
RN
RP
RC
RX
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RT
RT
RT
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RN
[5]
RN
RP
RC
RX
RX
RX
RA
RA
RT
RT
RT
RL
RN

NUCLEOTIDE SEQUENCE.
MEDLINE=21153566; PubMed=11254561;
DOI=10.1128/IAI.69.4.2083-2091.2001;
Onishi N., Kikihisa Y., Unver A.;
"Analysis of transcriptionally active gene clusters of major outer
membrane protein multigene family in *Escherichia canis* and *E.*
chaffeensis.";
Infect. Immun. 69:2083-2091(2001).
[5]

RP NUCLEOTIDE SEQUENCE.
RC SPAIN:Venezuela, Arizona, California, and New Mexico;
RX MEDLINE=22461955; Pubmed=12574308; DOI=10.1128/JCM.41.2.886-888.2003;
RA Felek S., Greene R., Rikhihsa Y.;
RT "Transcriptional Analysis of p30 Major Outer Membrane Protein Genes of
RT *Escherichia canis* in Naturally Infected Ticks and Sequence Analysis of
RT p30-10 of *E. canis* from Diverse Geographic Regions.";

RL	J. Clin. Microbiol.	41:885-888	(2003).
DR	EWBL;	AF082744;	AAG14357.1; -; Genomic DNA.
DR	EWBL;	AF078553;	AAK28696.1; -; Genomic DNA.
DR	EWBL;	AF324792;	AAK31312.1; -; Genomic DNA.
DR	EWBL;	AF28512;	AAO41109.1; -; Genomic DNA.
DR	EWBL;	AF528515;	AAO41112.1; -; Genomic DNA.
DR	EWBL;	AF528514;	AAO41111.1; -; Genomic DNA.
DR	EWBL;	AF528511;	AAO41108.1; -; Genomic DNA.
DR	Interpro;	IPR002566;	Surface Ag_msp4.
DR	Pfam;	PF01617;	Surface Ag_2.
SO	SEQUENCE	280 AA;	30562.MW; D1BB28B5AFOE6CA3 CRC64;

RESULT 3	
Q8G9D6_EHRCH	
ID Q8G9D6_EHRCH PRELIMINARY;	PRT; 283 AA.
AC Q8G9D6;	
DT 01-MAR-2003 (TrEMBLrel. 23, Created)	
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)	
DE 28kDa outer membrane protein gene 14.	
OS Ehrlichia chaffeensis.	
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;	
OC Anaplasmataceae; Ehrlichia.	
OX NCBI TaxID=945;	

RESULT 5	
Q8G812_EHRCH	
ID	Q8G812_EHRCH PRELIMINARY; PRT; 283 AA.
AC	Q8G812;
DT	01-MAR-2003 (T-EMBLrel. 23, Created)
DT	01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT	01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE	28kDa outer membrane protein gene 14.
OS	Ehrlichia chaffeensis.
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC	Anaplasmataceae; Ehrlichia.
OX	NCBI_TaxID=945;
RN	{1}
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=22384137; PubMed=12496165; DOI=10.1128/TAI.71.1.187-195.2003;

RA Cheng C., Paddock C.D., Ganta R.R.;
 RT "Molecular heterogeneity of Ehrlichia chaffeensis isolates determined
 by sequence analysis of the 28-kilodalton outer membrane protein genes
 and other regions of the genome.";
 RL Infect. Immun. 71:187-195(2003).
 DR EMBL: AF479839; AAO12959.1; -; Genomic_DNA.
 DR EMBL: AF479840; AAO12965.1; -; Genomic_DNA.
 DR InterPro: IPR002566; Surface Ag_msp4.
 DR Pfam: PF01617; Surface Ag 2; 1.
 SQ SEQUENCE 283 AA; 31069 MW; AEA8B2833E02631F CRC64;

Query Match 72.1%; Score 98; DB 2; Length 283;
 Best Local Similarity 69.2%; Pred. No. 7e-06;
 Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 PINGTNSLTQKVFGLKKGDDITKDD 26
 ||||| :|||:|||||:|||||:
 Db 64 PINGNTAITKVFGLKKGDDIAHQGD 89

RESULT 6
 ID O85358_EHRCH PRELIMINARY; PRT; 283 AA.
 AC O85358; O52103;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE 28kDa outer membrane protein gene 14 (Major outer membrane protein
 OMP-1B).
 GN Name=omp-1B;
 OS Ehrlichia chaffeensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 OX NCBI_TaxID=945;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=983211180; PubMed=9647746; DOI=10.1006/bbrc.1998.8844;
 RA Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burrridge M.J.,
 RA Alleman A.R.;
 RT "Molecular characterization of a 28 kDa surface antigen gene family of
 the tribe Ehrlichiae.";
 RL Biochem. Biophys. Res. Commun. 247:636-643(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22384137; PubMed=12496165; DOI=10.1128/IAI.71.1.187-195.2003;
 RA Cheng C., Paddock C.D., Ganta R.R.;
 RT "Molecular heterogeneity of Ehrlichia chaffeensis isolates determined
 by sequence analysis of the 28-kilodalton outer membrane protein genes
 and other regions of the genome.";
 RL Infect. Immun. 71:187-195(2003).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Cheng C., Paddock C.D., Ganta R.R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Arkansas;
 RX MEDLINE=98084455; PubMed=9423849;
 RA Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
 RT "Immunodominant major outer membrane proteins of Ehrlichia chaffeensis
 are encoded by a polymorphic multigene family.";
 RL Infect. Immun. 66:132-139(1998).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Arkansas;
 RX MEDLINE=21153566; PubMed=11254561;
 RA DOI=10.1128/IAI.69.4.2083-2091.2001;
 RA Ohashi N., Rikihisa Y., Unver A.;
 RT "Analysis of transcriptionally active gene clusters of major outer
 membrane protein multigene family in Ehrlichia canis and E.
 chaffeensis.";
 RL Infect. Immun. 69:2083-2091(2001).
 DR EMBL: AF479833; AAO12929.1; -; Genomic_DNA.

DR EMBL: U72291; AAC02936.1; -; Genomic_DNA.
 DR EMBL: AF479834; AAO12933.1; -; Genomic_DNA.
 DR InterPro: IPR002566; Surface Ag_msp4.
 DR Pfam: PF01617; Surface Ag 2; 1.
 SQ SEQUENCE 283 AA; 31017 MW; DCBCF652B771C95D CRC64;

Query Match 71.3%; Score 97; DB 2; Length 283;
 Best Local Similarity 78.3%; Pred. No. 9.8e-06;
 Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTQKVFGLKKGDDITK 23
 ||||| :|||:|||||:|||||:
 Db 64 PINGNTSITKVFGLKKGDDIAQ 86

RESULT 7
 ID Q5W5Y1_EHRRU PRELIMINARY; PRT; 282 AA.
 AC Q5W5Y1;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE MAP1-1.
 GN Name=map1-1;
 OS Ehrlichia ruminantium (Cowdria ruminantium).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 OX NCBI_TaxID=779;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Senegal;
 RX MEDLINE=22035368; PubMed=12039046; DOI=10.1016/S0378-1119(02)00408-0;
 RA Bekker C.P., Bell-Sakyi L., Paxton E.A., Martinez D., Bensaid A.,
 RA Jongejan F.;
 RT "Transcriptional analysis of the major antigenic protein 1 multigene
 family of Cowdria ruminantium.";
 RL Gene 285:193-201(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Senegal;
 RX PubMed=15995193; DOI=10.1128/JB.187.14.4782-4791.2005;
 RA Bekker C.P., Postigo M., Taoufik A., Bell-Sakyi L., Ferraz C.,
 RA Martinez D., Jongejan F.;
 RT "Transcription Analysis of the Major Antigenic Protein 1 Multigene
 Family of Three In Vitro-Cultured Ehrlichia ruminantium Isolates.";
 RL J. Bacteriol. 187:4782-4791(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Senegal;
 RA Bekker C.P.J., Taoufik A., Jongejan F.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF319940; AAV54088.2; -; Genomic_DNA.
 SQ SEQUENCE 282 AA; 31097 MW; 3D619510E7393EBB CRC64;

Query Match 66.2%; Score 90; DB 2; Length 282;
 Best Local Similarity 69.2%; Pred. No. 0.00011;
 Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PINGTNSLTQKVFGLKKGDDITKDD 26
 ||||| :|||:|||||:|||||:
 Db 64 PVYKDSPTKVFGLKKGDSITKYS 89

RESULT 8
 ID Q9R443_EHRRU PRELIMINARY; PRT; 282 AA.
 AC Q9R443;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Major antigenic protein 1 like protein.
 OS Ehrlichia ruminantium (Cowdria ruminantium).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;

[illegible]

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Map1-related protein.
 GN OrderedLocusNames=ERGA_CDS_09150;
 OS Ehrlichia ruminantium (strain Gardel).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 OX NCBI_TaxID=302409;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Gardel;
 RA Frutos R., Ferraz C., Bensaid A., Eychenie S., Kandassami Y., Viari A.,
 RA Chantal I., Morgat A., Colissac E., Vachieri N., Demaille J., Viari A.,
 RA Martinez D.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR925677; CA128367.1; -; Genomic_DNA.
 DR InterPro; IPR002566; Surface_Ag_msp4.
 DR Pfam; PF01617; Surface_Ag_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 304 AA; 33925 MW; 009338D2B65AE800 CRC64;

 Query Match 63.2%; Score 86; DB 2; Length 304;
 Best Local Similarity 65.4%; Pred. No. 0.00044;
 Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

 QY 1 PINGTSLTKKVFGLKKGDKITKDD 26
 Db 86 PVYKDSPTKKVFGLKKEGSIKYSD 111

 RESULT 13
 QSFCD9_EHRRW
 ID QSFCD9_EHRRW PRELIMINARY; PRT; 304 AA.
 AC QSFCD9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Map1-related protein.
 GN OrderedLocusNames=ERWE_CDS_09240;
 OS Ehrlichia ruminantium (strain Welgevonden).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 OX NCBI_TaxID=254945;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Welgevonden;
 RA Frutos R., Ferraz C., Bensaid A., Eychenie S., Kandassami Y., Viari A.,
 RA Chantal I., Morgat A., Colissac E., Vachieri N., Demaille J., Viari A.,
 RA Martinez D.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR925678; CA127418.1; -; Genomic_DNA.
 DR InterPro; IPR002566; Surface_Ag_msp4.
 DR Pfam; PF01617; Surface_Ag_2; 1.
 SQ SEQUENCE 304 AA; 33925 MW; 009338D2B65AE800 CRC64;

 Query Match 63.2%; Score 86; DB 2; Length 304;
 Best Local Similarity 65.4%; Pred. No. 0.00044;
 Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

 QY 1 PINGTSLTKKVFGLKKGDKITKDD 26
 Db 86 PVYKDSPTKKVFGLKKEGSIKYSD 111

 RESULT 14
 Q8A3S3_BACTN
 ID Q8A3S3_BACTN PRELIMINARY; PRT; 238 AA.
 AC Q8A3S3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase.
 GN OrderedLocusNames=BT2881;

OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 299:2074-2076(2003).
 DR EMBL; AS016937; AA077987.1; -; Genomic DNA.
 DR GO; GO:0050518; F:2-C-methyl-D-erythritol 4-phosphate cytidyl. . .; IEA.
 DR GO; GO:0008699; F:4-diphosphocytidyl-2C-methyl-D-erythritol s. . .; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
 DR InterPro; IPR008233; DPCME_synth.
 DR InterPro; IPR001228; ISPD_synthase.
 DR Pfam; PF01128; ISPD; 1.
 DR PIRSF; PIRSF006765; DPCME synth; 1.
 DR PROSITE; PS01295; ISPD; UNKNOWN 1.
 KW Complete proteome; Nucleotidyltransferase; Transferase.
 SQ SEQUENCE 238 AA; 26323 MW; 8C565Cf8E8DE768 CRC64;

 Query Match 47.1%; Score 64; DB 2; Length 238;
 Best Local Similarity 52.0%; Pred. No. 0.6;
 Matches 13; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

 QY 2 INGTSLTKKVFGLKKGDKITKDD 26
 Db 80 INQESISNGIYGLKKG--VKDD 102

 RESULT 15
 Q7R7D4_PLAYO
 ID Q7R7D4_PLAYO PRELIMINARY; PRT; 266 AA.
 AC Q7R7D4;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative Yir3 protein.
 GN Names=PY07653;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteu M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin H.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01002851; EAA20157.1; -; Genomic_DNA.
 DR InterPro; IPR006477; Yir_bir_cir.
 DR Pfam; PF06022; Yir_bir_Yir.
 DR TIGRFAMs; TIGR01590; Yir-bir-cir_Pla; 1.
 SQ SEQUENCE 266 AA; 31613 MW; AC785DSA383F8C5E CRC64;

 Query Match 41.9%; Score 57; DB 2; Length 266;

Best Local Similarity 50.0%; Pred. No. 7.2;
Matches 12; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 2 INGTNSLTKKVFLKXKGDITKKD 25
Db 165 LEGDNEFVKKYDQLKKDSINIKDD 188

Search completed: January 24, 2006, 11:46:49
Job time : 21.5425 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:36:23 ; Search time 4.07843 Seconds
(without alignments)
613.382 Million cell updates/sec

Title: US-10-680-349-42_COPY_61_86
Perfect score: 136
Sequence: 1 PINGNSLTQKVFGLKDDITFKDD 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53.5	39.3	2523	T18477	hypothetical prote
2	51	37.5	559	T00714	hypothetical prote
3	50	36.8	284	I40882	major antigenic pr
4	49.5	36.4	521	B71717	hypothetical prote
5	49.5	36.4	1650	T18444	hypothetical prote
6	49	36.0	345	D91201	type III secretion
7	49	36.0	345	H86047	escu (imported) -
8	49	36.0	363	F97092	probable membrane
9	49	36.0	1245	S51255	probable membrane
10	48.5	35.7	608	T02299	hypothetical prote
11	48.5	35.7	1092	JN0635	neural cell adhesi
12	48.5	35.7	1127	E71156	endopeptidase La h
13	48	35.3	155	T29928	hypothetical prote
14	48	35.3	274	H83707	bacitracin resist
15	48	35.3	427	F75169	serine hydroxymeth
16	48	35.3	635	B72215	hypothetical prote
17	48	35.3	900	G87431	pyruvate phosphate
18	48	35.3	908	AE2675	pyruvate, orthophos
19	48	35.3	930	F73431	pyruvate, phosphat
20	48	35.3	933	C97457	pyruvate, phosphat
21	47.5	34.9	295	I53296	testis-specific es
22	47.5	34.9	564	A34325	juvenile-hormone e
23	47.5	34.9	881	F72397	pyruvate, phosphat
24	47	34.6	427	F71045	probable serine hy
25	46.5	34.2	833	H72205	maltoase ABC transp
26	46.5	34.2	879	AC1308	pyruvate phosphate
27	46.5	34.2	879	AC1680	pyruvate, phosphat
28	46.5	34.2	947	KIZMPO	pyruvate, phosphat
29	46.5	34.2	947	T02979	pyruvate, phosphat

30	46.5	34.2	949	1	S55478	pyruvate, phosphat
31	46.5	34.2	953	2	S56650	pyruvate, phosphat
32	46.5	34.2	953	2	S12894	pyruvate, phosphat
33	46.5	34.2	955	2	S56649	pyruvate, phosphat
34	46.5	34.2	956	2	S53297	pyruvate, phosphat
35	46.5	34.2	960	2	A71420	hypothetical prote
36	46	33.8	225	2	T21094	hypothetical prote
37	46	33.8	440	2	T01115	probable protein d
38	46	33.8	517	2	A71707	lipopolysaccharide
39	46	33.8	631	2	S70908	transferrin-bindin
40	46	33.8	840	1	KIOAPO	pyruvate, phosphat
41	46	33.8	1123	2	T28139	PK4 protein kinase
42	46	33.8	1505	2	T31418	synaptonemal compl
43	46	33.8	2469	2	H36812	hypothetical prote
44	45.5	33.5	70	2	B64497	hypothetical prote
45	45.5	33.5	72	2	C95929	hypothetical expor

ALIGNMENTS

RESULT 1

T18477
hypothetical protein C0485w - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18477
R:Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z18937
A:Accession: T18477
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-2523 <Law>
A:Cross-references: UNIPROT:O77365; UNIPARC:UPI000017CC31; EMBL:AL008970; NID:e1407852; I

RESULT 2

T00714
hypothetical protein F22013.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00714
R:Shinn, P.; Buehler, E.; Dewar, K.; Peng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Con
eologis, A.; Ecker, J.R.
submitted to the EMBL Data Library, April 1998
A:Description: Genomic sequence for Arabidopsis thaliana BAC F22013.
A:Reference number: Z14200
A:Accession: T00714
A:Status: translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-559 <SH1>
A:Cross-references: UNIPROT:Q9FRS4; UNIPARC:UPI00000A4F36; EMBL:AC003981; NID:g3063438; I

Query Match 39.3%; Score 53.5; DB 2; Length 2523;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 15; Conservative 1; Mismatches 9; Indels 5; Gaps 1;

Qy 2 INGTNSLTQKVFGLKDD----GDITKKDD 26
Db 1822 INKNDINKDDINKKDDINKKDDINKKDD 1851

RESULT 2

T00714
hypothetical protein F22013.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00714
R:Shinn, P.; Buehler, E.; Dewar, K.; Peng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Con
eologis, A.; Ecker, J.R.
submitted to the EMBL Data Library, April 1998
A:Description: Genomic sequence for Arabidopsis thaliana BAC F22013.
A:Reference number: Z14200
A:Accession: T00714
A:Status: translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-559 <SH1>
A:Cross-references: UNIPROT:Q9FRS4; UNIPARC:UPI00000A4F36; EMBL:AC003981; NID:g3063438; I

Query Match 37.5%; Score 51; DB 2; Length 559;
Best Local Similarity 44.4%; Pred. No. 21;
Matches 12; Conservative 3; Mismatches 8; Indels 4; Gaps 1;

```
QY 4 GTNSLTK----KVFGFKKGGDITKKDD 26
||| : ||| ||| ||| : ||| :
Db 78 GTNLRAVVKPMQKFGLLSSDGPITENDE 104
||| : ||| ||| ||| ||| : ||| :

RESULT 3
I40882
major antigenic protein - heartwater rickettsia
C:Species: Cowdria ruminantium (heartwater rickettsia)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40882; S42827
R:van Vliet, A.H.; Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.
Infect. Immun. 62, 1451-1456, 1994
A:Title: Molecular cloning, sequence analysis, and expression of the gene encoding the
A:Reference number: I40882; MUID:94178956; PMID:8132352
A:Accession: I40882
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-284 <RES>
A:Cross-references: UNIPROT:Q46327; UNIPARC:UPI00000B9A44; EMBL:X74250; NID:9454266; PID
C:Genetics:
A:Gene: map1

Query Match 36.8%; Score 50; DB 2; Length 284;
Best Local Similarity 73.3%; Pred. No. 14;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 TKKVFGLKKGGDITK 23
||| ||| ||| ||| ||| |||
Db 63 TKAVFGLKKDGDGVK 77

RESULT 4
B71717
hypothetical protein RP083 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: B71717
R:Anderson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichertz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: B71717
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-521 <AND>
A:Cross-references: UNIPROT:Q9ZE64; UNIPARC:UPI00000C114A; GB:AJ235270; GB:AJ235269; NID
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: RP083

Query Match 36.4%; Score 49.5; DB 2; Length 521;
Best Local Similarity 47.8%; Pred. No. 32;
Matches 11; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 3 NGTNSLTKKVFGLKKGGDITKKD 25
| | : : | | ||| ||| : |
Db 83 NLNNKILEKIF-LKDDGTITEQD 104

RESULT 5
T18444
hypothetical protein C0385c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18444
R:Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z18935
A:Accession: T18444
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1650 <LAW>
```

```
A:Cross-references: UNIPROT:O77328; UNIPARC:UPI00000748ED; EMBL:Z98547; NID:e1325376; PID
C:Genetics:
A:Map position: 3
A:Introns: 1597/3; 1625/3
A:Note: C0385c

Query Match 36.4%; Score 49.5; DB 2; Length 1650;
Best Local Similarity 57.1%; Pred. No. 11e+02;
Matches 12; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 6 NSLTKKVFGLKKGGDITKKDD 26
::| ||| :||| ||| |||
Db 932 STLEKKVF-VKCDNVITNDD 951

RESULT 6
D91201
type III secretion system Escu protein [imported] - Escherichia coli (strain O157:H7, su1
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: D91201
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D91201
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <HAY>
A:Cross-references: UNIPROT:O85640; UNIPARC:UPI00000D00D0; GB:BA000007; PIDN:BA038003.1;
A:Experimental source: strain O157:H7, substrain RIND 0509952
C:Genetics:
A:Gene: EC94580
C:Superfamily: flagellar biosynthetic protein flhB; flhB carboxyl-terminal homology

Query Match 36.0%; Score 49; DB 2; Length 345;
Best Local Similarity 52.9%; Pred. No. 25;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 10 KKVFGLKKGGDITKKDD 26
|| : ||| ||| :| :
Db 11 KKLRDLKKKGDVTKSEE 27

RESULT 7
H86047
escU [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H86047
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H86047
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <STO>
A:Cross-references: UNIPROT:O85640; UNIPARC:UPI00000D00D0; GB:AE005174; NID:g12518474; P1
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: escU
C:Superfamily: flagellar biosynthetic protein flhB; flhB carboxyl-terminal homology

Query Match 36.0%; Score 49; DB 2; Length 345;
Best Local Similarity 52.9%; Pred. No. 25;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 10 KKVFGLKKGGDITKKDD 26
|| : ||| ||| :| :
Db 11 KKLRDLKKKGDVTKSEE 27
```

A:Reference number: Z14637
 A:Accession: T02299
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-608 <LAW>
 A:Cross-references: UNIPROT:O60378; UNIPARC:UPI0000073023; EMBL:AC004475; NID:G2988396; I
 R:Kohrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: Z23037
 A:Accession: T46353
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 217-608 <AAA>
 A:Cross-references: UNIPARC:UPI000007056F; EMBL:AL137286
 A:Experimental source: adult testis; clone DKFPz434E2216
 C:Genetics:
 A:Map position: 19
 A:Introns: 58/1; 84/1; 143/3; 185/1; 218/3; 260/1; 378/3; 414/2; 473/3; 509/2; 558/1; 601
 A:Note: DKFPz434E2216.1

Query Match	35.7%	Score 48.5;	DB 2;	Length 608;
Best Local Similarity	33.3%	Pred. No. 53;		
Matches	9;	Conservative	9;	Mismatches 8; Indels 1; Gaps 1;
QY	1	PIN-GTNSLTKKVFGKKGDDITKKDD	26	
DB	554	PVNGTITVDGAGFGIDRPAELSKEDD	580	

RESULT 11
 JN0635
 neural cell adhesion molecule 2 precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C:Accession: JN0635
 R:Tonissen, K.F.; Krieg, P.A.
 Gene 127, 243-247, 1993
 A:Title: Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus laevis are exi
 A:Reference number: JN0635; MUID:93273239; PMID:7684721
 A:Accession: JN0635
 A:Molecule type: mRNA
 A:Residues: 1-1092 <TON>
 A:Cross-references: UNIPROT:P36335; UNIPARC:UPI000012FDC7; GB:M76710; NID:G214611; PIDN: f
 C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mole
 C:Genetics:
 A:Gene: NCAM2
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C:Keywords: alternative splicing; cell adhesion; duplication; heparin binding; sialoglyc
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-1092/Product: neural cell adhesion molecule 2 #status predicted <NCA>
 F:120-705/Domain: extracellular #status predicted <EXT>
 F:34-95/Domain: immunoglobulin homology <IMM1>
 F:129-188/Domain: immunoglobulin homology <IMM2>
 F:149-153/Region: heparin binding #status predicted
 F:158-162/Region: heparin binding #status predicted
 F:317-381/Domain: immunoglobulin homology <IMM3>
 F:413-475/Domain: immunoglobulin homology <IMM4>
 F:512-589/Domain: fibronectin type III repeat homology <FN3A>
 F:613-680/Domain: fibronectin type III repeat homology <FN3B>
 F:706-723/Domain: transmembrane #status predicted <TM>
 F:724-1092/Domain: intracellular #status predicted <INT>
 F:41-93,136-186,232-282,379,420-473/Disulfide bonds: #status predicted
 F:219,310,341,417,443,472/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match	35.7%	Score 48.5;	DB 1;	Length 1092;
Best Local Similarity	41.9%	Pred. No. 98;		
Matches	13;	Conservative	3;	Mismatches 10; Indels 5; Gaps 1;
QY	1	PINGTNSLTKKVFGKKGDD	26	
DB	591	PVKGPSAPKLVLGHLSBDGNSIKVDIIKKDD	621	

A:Reference number: Z14637
 A:Accession: T02299
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-608 <LAW>
 A:Cross-references: UNIPROT:O60378; UNIPARC:UPI0000073023; EMBL:AC004475; NID:G2988396; I
 R:Kohrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: Z23037
 A:Accession: T46353
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 217-608 <AAA>
 A:Cross-references: UNIPARC:UPI000007056F; EMBL:AL137286
 A:Experimental source: adult testis; clone DKFPz434E2216
 C:Genetics:
 A:Map position: 19
 A:Introns: 58/1; 84/1; 143/3; 185/1; 218/3; 260/1; 378/3; 414/2; 473/3; 509/2; 558/1; 601
 A:Note: DKFPz434E2216.1

Query Match	36.0%	Score 49;	DB 2;	Length 363;
Best Local Similarity	50.0%	Pred. No. 26;		
Matches	11;	Conservative	3;	Mismatches 4; Indels 1;
QY	9	TKKVF----GLKKGDDITKKDD	26	
DB	152	TGKYVPLDGLKGDGVKNKTD	173	

RESULT 9
 S51255
 probable membrane protein YDR104c - yeast (Saccharomycetes cerevisiae)
 N:Alternate names: hypothetical protein YD8557.13c
 C:Species: Saccharomycetes cerevisiae
 C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
 C:Accession: S51255
 R:Murphy, L.; Harris, D.
 submitted to the EMBL Data Library, January 1995
 A:Reference number: S51243
 A:Accession: S51255
 A:Molecule type: DNA
 A:Residues: 1-1245 <MUR>
 A:Cross-references: UNIPROT:Q03868; UNIPARC:UPI000006B2F3; EMBL:Z47746; NID:G633627; PID
 C:Genetics:
 A:Gene: SGD:SPO71; MIPS:YDR104C
 A:Cross-references: SGD:S0002511
 A:Map position: 4R
 C:Superfamily: Saccharomycetes cerevisiae probable membrane protein YDR104c
 C:Keywords: transmembrane protein
 F:1045-1061/Domain: transmembrane #status predicted <TM>

Query Match	36.0%	Score 49;	DB 2;	Length 1245;
Best Local Similarity	52.4%	Pred. No. 95;		
Matches	11;	Conservative	2;	Mismatches 8; Indels 0; Gaps 0;
QY	5	TNSLTKKVFGKKGDDITKKD	25	
DB	440	TNSLTNATKVKRTGQILKKE	460	

RESULT 10
 T02299
 hypothetical protein F23858.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T02299; T46353
 R:Lamerdin, J.E.; McCreedy, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.; C
 ; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, C.; Andreise, T.; Frankhei
 submitted to the EMBL Data Library, March 1998
 A:Authors: Duarte, S.; Lucas, S.; Bruce, R.; Thomas, P.; Quan, G.; Krommiller, B.; Arell
 A:Description: Sequence analysis of a human p1 clone containing the XRC9 DNA repair ge

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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:28:32 ; Search time 190.327 Seconds
(without alignments)
646.394 Million cell updates/sec

Title: US-10-680-349-42
Perfect score: 1462
Sequence: 1 MYKKILVRSALISLSILP.....ASVTLDVGYGGEIGMRFTF 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003s:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1462	100.0	280	5 AAU96116	Aau96116 Ehrlichia
2	1462	100.0	280	5 ABG77958	Abg77958 Ehrlichia
3	1462	100.0	280	6 ADA09781	Ada09781 E. canis
4	1462	100.0	280	9 ADW04274	Adw04274 Ehrlichia
5	1202.5	82.3	283	2 AAY06944	Aay06944 E. chaffe
6	1202.5	82.3	283	5 AAU96106	Aau96106 Ehrlichia
7	1202.5	82.3	283	5 AAU73413	Aau73413 Ehrlichia
8	1202.5	82.3	283	5 ABG77936	Abg77936 Ehrlichia
9	1202.5	82.3	283	6 ADA09737	Ada09737 E. chaffe
10	1202.5	82.3	283	9 ADW04230	Adw04230 Ehrlichia
11	715	48.9	165	2 AAY06970	Aay06970 E. canis
12	644.5	44.1	281	2 AAY06943	Aay06943 E. chaffe
13	644.5	44.1	281	5 AAU96105	Aau96105 Ehrlichia
14	644.5	44.1	281	5 AAU73418	Aau73418 Ehrlichia
15	644.5	44.1	281	5 ABG77935	Abg77935 Ehrlichia
16	642.5	43.9	281	6 ADA09735	Ada09735 E. chaffe
17	642.5	43.9	281	9 ADW04228	Adw04228 Ehrlichia
18	642.5	43.9	281	9 ADW04293	Adw04293 Ehrlichia
19	629.5	43.1	276	2 AAW51095	Aaw51095 Ehrlichia
20	629.5	43.1	276	3 AAB36189	Aab36189 Ehrlichia
21	629.5	43.1	276	4 AAU04199	Aau04199 Variable
22	622	42.5	286	2 AAW51092	Aaw51092 Ehrlichia
23	621	42.5	288	2 AAY06959	Aay06959 E. canis
24	621	42.5	288	5 ABG77950	Abg77950 Ehrlichia

25	621	42.5	288	6 ADA09765	Ada09765 E. canis
26	621	42.5	288	9 ADW04258	Adw04258 Ehrlichia
27	620	42.4	286	2 AAY06946	Aay06946 E. chaffe
28	620	42.4	286	3 AAB36186	Aab36186 Ehrlichia
29	620	42.4	286	4 AAU04196	Aau04196 Variable
30	620	42.4	286	5 AAU96108	Aau96108 Ehrlichia
31	620	42.4	286	5 AAU73415	Aau73415 Ehrlichia
32	620	42.4	286	5 ABG77938	Abg77938 Ehrlichia
33	620	42.4	286	6 ADA09741	Ada09741 E. chaffe
34	620	42.4	286	9 ADW04234	Adw04234 Ehrlichia
35	606	41.5	280	5 ABG77953	Abg77953 Ehrlichia
36	605	41.4	280	2 AAY06948	Aay06948 E. chaffe
37	605	41.4	280	5 AAU96110	Aau96110 Ehrlichia
38	605	41.4	280	5 ABG77940	Abg77940 Ehrlichia
39	605	41.4	280	6 ADA09745	Ada09745 E. chaffe
40	605	41.4	280	9 ADW04238	Adw04238 Ehrlichia
41	603	41.2	280	2 AAW51094	Aaw51094 Ehrlichia
42	603	41.2	280	3 AAB36188	Aab36188 Ehrlichia
43	603	41.2	280	4 AAU04198	Aau04198 Variable
44	603	41.2	280	5 AAU73417	Aau73417 Ehrlichia
45	601	41.1	280	2 AAY06962	Aay06962 E. canis

ALIGNMENTS

RESULT 1
AAU96116
ID AAU96116 standard; protein; 280 AA.
XX
AC AAU96116;
XX
DT 02-JUL-2002 (first entry)
XX
DE Ehrlichia canis p28-2.
XX
KW Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
XX
OS Ehrlichia canis.
XX
PN WO200222782-A2.
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-US028759.
XX
PR 12-SEP-2000; 2000US-00660587.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Walker DH, Yu X, McBride JW;
XX
WPI: 2002-351882/38.
DR N-PSDB; ABK68876.
XX
PT New recombinant homologous 28 kilodalton immunodominant protein from
PT Ehrlichia canis, useful for treating Ehrlichia canis infections.
PS Claim 16; Fig 14; 106pp; English.
XX
CC The invention relates to a recombinant homologous 28 kDa immunodominant
CC protein, p28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably
CC dispersed in a pharmaceutically acceptable carrier, is useful for
CC inhibiting E. canis infection in a subject. (I) is useful in the
CC development of vaccines and serodiagnostics that are particularly
CC effective for disease prevention and serodiagnosis. AAU96100-AAU96118
CC represent the 28-kDa antigen amino acid sequences of the invention
XX
SQ Sequence 280 AA;

Query Match 100.0%; Score 1462; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.1e-138; Indels 0; Gaps 0;
Matches 280; Conservative 0; Mismatches 0;

QY 1 MNYKKILVRSALISLMSILPYQSPADPVGSRDNDNKEGYISAKYNPSISHPRKFSABET 60
DB 1 MNYKKILVRSALISLMSILPYQSPADPVGSRDNDNKEGYISAKYNPSISHPRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKDGDITTKDDFTRVAPGIDFQNNLISGFGSGISGYSMDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKDGDITTKDDFTRVAPGIDFQNNLISGFGSGISGYSMDGPRIELE 120
QY 121 AAYQQFNPKNVTNDNDTNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQQFNPKNVTNDNDTNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVQKIGISYPIPTPEVSATFGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVQKIGISYPIPTPEVSATFGGYHGVGNK 240
QY 241 FEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280

RESULT 2
ABG77958
ID ABG77958 standard; protein; 280 AA.
XX AC ABG77958;
XX DT 15-NOV-2002 (first entry)
XX DE Ehrlichia canis outer membrane protein (P30F) #9.
XX KW Outer membrane protein; OMP; P30F; ehrlichiosis; infection.
XX OS Ehrlichia canis.
XX PN US2002120115-A1.
XX PD 29-AUG-2002.
XX PF 28-JAN-2002; 2002US-00059964.
XX PR 19-MAY-1999; 99US-00314701.
XX PA (RIKI/) RIKIHISA Y.
XX PA (OHAS/) OHASHI N.
XX PI Rikihisa Y, Ohashi N;
XX DR WPI: 2002-618954/66.
XX DR N-PSDB; ABS63299.
XX PT Isolated polynucleotide encoding an outer membrane protein of E.canis or
XX PT E.chaffeensis used in the diagnosis of infection.
XX PS Claim 10; Fig 30B; 49pp; English.

XX The invention relates to an isolated polynucleotide encoding an outer
XX membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used
XX in the diagnosis of infection. An infection such as human ehrlichiosis or
XX canine ehrlichiosis can be diagnosed by providing a serum sample from the
XX patient, providing a polypeptide or mixture of polypeptides, contacting
XX the sample with the polypeptide and assaying for the formation of a
XX complex between antibodies in the serum sample and the polypeptide, where
XX formation of a complex is indicative of infection with E. chaffeensis.
XX This sequence represents an Ehrlichia outer membrane protein of the
XX invention
SQ Sequence 280 AA;

Query Match 100.0%; Score 1462; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.1e-136;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYKKILVRSALISLMSILPYQSPADPVGSRDNDNKEGYISAKYNPSISHPRKFSABET 60
DB 1 MNYKKILVRSALISLMSILPYQSPADPVGSRDNDNKEGYISAKYNPSISHPRKFSABET 60
QY 61 PINGTNSLTKKVFGGLKKDGDITTKDDFTRVAPGIDFQNNLISGFGSGISGYSMDGPRIELE 120
DB 61 PINGTNSLTKKVFGGLKKDGDITTKDDFTRVAPGIDFQNNLISGFGSGISGYSMDGPRIELE 120
QY 121 AAYQQFNPKNVTNDNDTNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
DB 121 AAYQQFNPKNVTNDNDTNGEYKHFALSRKDMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
QY 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVQKIGISYPIPTPEVSATFGGYHGVGNK 240
DB 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVQKIGISYPIPTPEVSATFGGYHGVGNK 240
QY 241 FEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280
DB 241 FEKIPVITPVVLNDAPQTTASVTLDDVGYFGGEIGMRFTF 280

RESULT 3
ADA09781
ID ADA09781 standard; protein; 280 AA.
XX AC ADA09781;
XX DT 06-NOV-2003 (first entry)
XX DE E. canis outer membrane protein P30-10.
XX KW outer membrane protein; circulating leukocyte; monocytic ehrlichiosis;
XX KW Rocky Mountain spotted fever; canine ehrlichiosis; antigen.
XX OS Ehrlichia canis.
XX PN US6544517-B1.
XX PD 08-APR-2003.
XX PF 19-MAY-1999; 99US-00314701.
XX PR 18-SEP-1998; 98US-0100843P.
XX PA (OHIS) UNIV OHIO STATE RES FOUND.
XX PI Rikihisa Y, Ohashi N;
XX DR WPI: 2003-553952/52.
XX DR N-PSDB; ADA09780.

XX New isolated polynucleotide encoding outer membrane protein P30 of
XX Ehrlichia canis or its variant or fragment, useful for producing
XX Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins for
XX diagnosing and treating ehrlichiosis.
XX PS Disclosure; Fig 30; 105pp; English.
XX The invention relates to an isolated polynucleotide encoding a variant of
XX the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer
XX membrane protein of E. canis , or an antigenic fragment of the E. canis
XX P30 protein, or comprising a sequence which is the complement of
XX nucleotide 99 through nucleotide 672 of ADA09784. Also disclosed are E.
XX canis and E. chaffeensis outer membrane proteins and their encoding
XX nucleic acids. The polynucleotides are useful for producing E. canis or
XX E. chaffeensis outer membrane protein, for designing hybridisation probes
XX for isolating and identifying cDNA and genomic clones encoding the OMP
XX or its allelic forms, for designing primers for PCR. The polypeptides
XX encoded by the polynucleotide is useful for diagnosing human ehrlichiosis
XX (Rocky mountain spotted fever) or canine ehrlichiosis. The present
XX sequence represents an E. canis outer membrane protein.

SQ	Sequence 280 AA;	CC	proteins (OMP) of Ehrlichia chaffeensis (designated as OMP proteins) and Ehrlichia canis (designated as P30F proteins). The OMP polynucleotide is useful in preparing a composition for diagnosing, treating or preventing an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present sequence is the Ehrlichia canis P30F protein.
	Query Match		
	Best Local Similarity 100.0%; Score 1462; DB 6; Length 280;		
	Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGFYISAKYNPSISHFRKFSAEET 60	QY	1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGFYISAKYNPSISHFRKFSAEET 60
DB	1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGFYISAKYNPSISHFRKFSAEET 60	DB	1 MNYKKILVRSALISLMSILPYQSFADPVGSRDNDNKEGFYISAKYNPSISHFRKFSAEET 60
QY	61 PINGTNSLTKKVGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGYSMDGPRIELE 120	QY	61 PINGTNSLTKKVGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGYSMDGPRIELE 120
DB	61 PINGTNSLTKKVGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGYSMDGPRIELE 120	DB	61 PINGTNSLTKKVGLKKGDIKKDDFTRVAPGIDFQNNLISGFSIGYSMDGPRIELE 120
QY	121 AAYQQFNPKNTDNDTNGEYKHFALSRKDAMEDQQYVVLKNDGITFMSLMVNTCYDIT 180	QY	121 AAYQQFNPKNTDNDTNGEYKHFALSRKDAMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
DB	121 AAYQQFNPKNTDNDTNGEYKHFALSRKDAMEDQQYVVLKNDGITFMSLMVNTCYDIT 180	DB	121 AAYQQFNPKNTDNDTNGEYKHFALSRKDAMEDQQYVVLKNDGITFMSLMVNTCYDIT 180
QY	181 AEGVSFVPYACAGIGADLITIFKDLNLKFPAYQKIGISYPTPEVSFAFIGGYHGVGNK 240	QY	181 AEGVSFVPYACAGIGADLITIFKDLNLKFPAYQKIGISYPTPEVSFAFIGGYHGVGNK 240
DB	181 AEGVSFVPYACAGIGADLITIFKDLNLKFPAYQKIGISYPTPEVSFAFIGGYHGVGNK 240	DB	181 AEGVSFVPYACAGIGADLITIFKDLNLKFPAYQKIGISYPTPEVSFAFIGGYHGVGNK 240
QY	241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEGIMRFTF 280	QY	241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEGIMRFTF 280
DB	241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEGIMRFTF 280	DB	241 FEKIPVITPVVLNDAPQTTASVTLDVGYFGGEGIMRFTF 280
RESULT 4		RESULT 5	
ADW04274		AA06944	
ID	ADW04274 standard; protein; 280 AA.	ID	AA06944 standard; protein; 283 AA.
XX	ADW04274;	XX	AA06944;
XX	24-MAR-2005 (first entry)	XX	27-AUG-2003 (revised)
DE	Ehrlichia canis outer membrane protein (P30F), P30-10.	DT	05-JUL-1999 (first entry)
KW	DNA purification; diagnosis; outer membrane protein; OMP; P30F protein; infection; vaccine.	XX	E. chaffeensis OMP-1B protein.
OS	Ehrlichia canis.	DE	Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30; detection; dog.
FT	Key	XX	Ehrlichia chaffeensis.
FT	Peptide 1..25	XX	WO9913720-A1.
FT	Protein 26..280	PN	25-MAR-1999.
FT	/note= "Ehrlichia canis mature OMP protein"	XX	18-SEP-1998; 98WO-US019600.
XX	US2004265334-A1.	XX	19-SEP-1997; 97US-0059353F.
PN	30-DEC-2004.	XX	(OHIS) UNIV OHIO STATE.
XX	29-JUL-2004; 2004US-00901774.	XX	Rikihisa Y, Ohashi N;
XX	18-SEP-1998; 98US-0100843P.	PI	WPI; 1999-254290/21.
PR	19-MAY-1999; 99US-00314701.	DR	N-PSDB; AAX34744.
PR	28-JAN-2002; 2002US-00059964.	XX	Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis.
XX	(RIKI/) RIKIHISA Y.	XX	Claim 12; Fig 4B; 55pp; English.
PA	(OHAS/) OHASHI N.	XX	The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in
PI	Rikihisa Y, Ohashi N;	XX	Claim 10; SEQ ID NO 48; 122pp; English.
XX	WPI; 2005-064871/07.	XX	The invention relates to nucleic acid sequences encoding outer membrane
XX	N-PSDB; ADW04273.	XX	
XX	New polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis, useful in preparing a composition for diagnosing or preventing E. canis or E. chaffeensis infection.		
XX	Claim 10; SEQ ID NO 48; 122pp; English.		
XX	The invention relates to nucleic acid sequences encoding outer membrane		

CC consist of proteins shown in AAU06959-970. The proteins and genes are
CC used to detect E. chaffeensis in patients and E. canis in dogs. (Updated
CC on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 283 AA;
Query Match 82.3%; Score 1202.5; DB 2; Length 283;
Best Local Similarity 79.5%; Pred. No. 3e-112;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;
QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSR---TNDNKEGFYISAKYNPSISHPRKFS 57
DB 1 MNYKKIFVSSALISLMSILPYQSFADPVTSNDTGINDSREGFYISVKYNPSISHPRKFS 60
QY 58 EETPINGTNSLTKKVFGELKKDGDITKKDFTTRVAPGIDFQNNLISGFSGSGYSMDGPRI 117
DB 61 EEAINGNTSITKKVFGELKKDGDIAQSANFNRTDPALEFQNNLISGFSGSGIYAMDGPRI 120
QY 118 ELEAAVQOFPNPNNDTNGEYKHFALSRKAMEDQVYVVKNDGITFMSLVNTCY 177
DB 121 ELEAAVQKFDKPNPNNDTNGSDYYKYFGLSREDAIAADKKYVVKNEGITFMSLVNTCY 180
QY 178 DITAEGVSPVPYACAGIGADLITIFKDLNLKFAVQKIGISYPIITPEVSAPFIGGYHGV 237
DB 181 DITAEGVPIPYACAGVADLINVFDNLKFSYQKIGISYPIITPEVSAPFIGGYHGV 240
QY 238 GNNFKIPVITPVLVNDAPQTTASVTLVDVGFGEIGMRFTF 280
DB 241 GNNFNKIPVITPVLVLEGAPQTTASVTLVDVGFGEVGVRTTF 283

RESULT 6
AAU96106
ID AAU96106 standard; protein; 283 AA.
XX AC AAU96106;
DT 07-AUG-2003 (revised)
DT 02-JUL-2002 (first entry)
XX Ehrlichia chaffeensis OMP-1B.
XX Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
XX Ehrlichia chaffeensis.
XX WO200222782-A2.
XX 21-MAR-2002.
XX 12-SEP-2001; 2001WO-US028759.
XX 12-SEP-2000; 2000US-00660587.
XX (RERE-) RES DEV FOUND.
XX Walker DH, Yu X, McBride JW;
XX WPI; 2002-351882/38.
XX New recombinant homologous 28 kilodalton immunodominant protein from
XX Ehrlichia canis, useful for treating Ehrlichia canis infections.
XX Example 3; Fig 3; 106pp; English.
XX The invention relates to a recombinant homologous 28 kDa immunodominant
XX protein, P28, (I) of Ehrlichia canis. (I), a 28-kDa antigen preferably
XX dispersed in a pharmaceutically acceptable carrier, is useful for
XX inhibiting E. canis infection in a subject. (I) is useful in the
XX development of vaccines and serodiagnostics that are particularly
XX effective for disease prevention and serodiagnosis. AAU96100-AAU96118
XX represent the 28-kDa antigen amino acid sequences of the invention.
XX (Updated on 07-AUG-2003 to correct OS field.)

XX SQ Sequence 283 AA;
Query Match 82.3%; Score 1202.5; DB 5; Length 283;
Best Local Similarity 79.5%; Pred. No. 3e-112;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;
QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSR---TNDNKEGFYISAKYNPSISHPRKFS 57
DB 1 MNYKKIFVSSALISLMSILPYQSFADPVTSNDTGINDSREGFYISVKYNPSISHPRKFS 60
QY 58 EETPINGTNSLTKKVFGELKKDGDITKKDFTTRVAPGIDFQNNLISGFSGSGYSMDGPRI 117
DB 61 EEAINGNTSITKKVFGELKKDGDIAQSANFNRTDPALEFQNNLISGFSGSGIYAMDGPRI 120
QY 118 ELEAAVQOFPNPNNDTNGEYKHFALSRKAMEDQVYVVKNDGITFMSLVNTCY 177
DB 121 ELEAAVQKFDKPNPNNDTNGSDYYKYFGLSREDAIAADKKYVVKNEGITFMSLVNTCY 180
QY 178 DITAEGVSPVPYACAGIGADLITIFKDLNLKFAVQKIGISYPIITPEVSAPFIGGYHGV 237
DB 181 DITAEGVPIPYACAGVADLINVFDNLKFSYQKIGISYPIITPEVSAPFIGGYHGV 240
QY 238 GNNFKIPVITPVLVNDAPQTTASVTLVDVGFGEIGMRFTF 280
DB 241 GNNFNKIPVITPVLVLEGAPQTTASVTLVDVGFGEVGVRTTF 283

RESULT 7
AAU73413
ID AAU73413 standard; protein; 283 AA.
XX AC AAU73413;
DT 12-MAR-2002 (first entry)
XX Ehrlichia chaffeensis outer membrane protein P28-14.
XX Ehrlichia chaffeensis outer membrane protein; P28; antibiotic; vaccine.
XX Ehrlichia chaffeensis.
XX WO200183699-A2.
XX 08-NOV-2001.
XX 01-MAY-2001; 2001WO-US013997.
XX 01-MAY-2000; 2000US-0201035P.
XX (RERE-) RES DEV FOUND.
XX Walker DH, Yu X;
XX WPI; 2002-066527/09.
XX Novel Ehrlichia chaffeensis 28-kDa outer membrane protein, designated P28
XX useful as a vaccine against Ehrlichia chaffeensis.
XX Disclosure; Fig 2; 97pp; English.
XX The invention relates to isolated and purified 28-kDa outer membrane
XX proteins (P28-1 to P28-21) of Ehrlichia chaffeensis. P28 proteins are
XX encoded by a 28kDa outer membrane protein multigene family. P28 proteins
XX are useful as a vaccine against E.chaffeensis. DNA encoding P28 is useful
XX for transfecting a host cell. AAU73400-AAU73420 represent Ehrlichia
XX chaffeensis P28 outer membrane proteins of the invention
XX SQ Sequence 283 AA;
Query Match 82.3%; Score 1202.5; DB 5; Length 283;
Best Local Similarity 79.5%; Pred. No. 3e-112;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

Qy	1	MYXKILVRSALISLMSILPYQSFADPVGSR---TNDNKEGFYISAKYNPSISGHPRKFS4	57
Db	1	MYXKILFVRSALISLMSILPYQSFADPVTSDTGTINDSREGFYISVKNPSISGHPRKFS4	60
Qy	58	ETPTINGTSLTKYFGLKKOGDIPKDDPFRVAPGIDFQNNLISFGSGSIGYAMDGPRI	117
Db	61	BEAPINGNTSITKVFGLKKOGDIAQSANFRVTDPALEFQNNLISFGSGSIGYAMDGPRI	120
Qy	118	ELEAAVQQNPKNNTDNGEYKHFALSRKQAMEDQQVVLKNDGIFTMSLWNTCY	177
Db	121	ELEAAVQKEDAKNPNDNTSGDYKYFGLSREDAIADKKTVVLKNEGIFTMSLWNTCY	180
Qy	178	DITAEGVSPVPACAGIGADLITIPKDLNLKFAVGKIGISYPIPTPEVSAFIGYVHGVI	237
Db	181	DITAEGVPIPIACAGVGNDLINVFKDFNLKFSVQKIGISYPIPTPEVSAFIGYTHGVI	240
Qy	238	GNNKEKIPVITPVLVNDAPQTTASVTLVDGYFGGEIGMRFTF	280
Db	241	GNNFNKIPVITPWLLEGAPQTTASVLTIDTGYFGGEGVGRFTF	283

RESULT 8	
ABG77936	
ID	ABG77936 standard; protein; 283 AA.
XX	
XX	ABG77936;
XX	
XX	
XX	15-NOV-2002 (first entry)
XX	
XX	Ehrlichia chaffeensis outer membrane protein (OMP) #2.
DE	
XX	
KW	Outer membrane protein; OMP; P30F; ehrlichiosis; infection.
XX	
OS	Ehrlichia chaffeensis.
XX	
PN	US2002120115-A1.
XX	
PD	29-AUG-2002.
XX	
XX	28-JAN-2002; 2002US-00059964.
PF	
XX	
PR	19-MAY-1999; 99US-00314701.
XX	
PA	(RIKI/) RIKIHISA Y.
PA	(OHAS/) OHASHI N.
XX	
PI	Rikihisa Y, Ohashi N;
XX	
XX	
DR	WPI; 2002-618954/66.
DR	N-PSDB; ABS63277.
XX	
PT	Isolated polynucleotide encoding an outer membrane protein of E.canis or
PT	E.chaffeensis used in the diagnosis of infection.
XX	
PS	Disclosure; Fig 4B; 49pp; English.
XX	
CC	The invention relates to an isolated polynucleotide encoding an outer
CC	membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used
CC	in the diagnosis of infection. An infection such as human ehrlichiosis or
CC	canine ehrlichiosis can be diagnosed by providing a serum sample from the
CC	patient, providing a polypeptide or mixture of polypeptides, contacting
CC	the sample with the polypeptide and assaying for the formation of a
CC	complex between antibodies in the serum sample and the polypeptide, where
CC	formation of a complex is indicative of infection with E. chaffeensis.
CC	This sequence represents an Ehrlichia outer membrane protein of the
CC	invention
XX	
SQ	Sequence 283 AA;

Qy	1	MNYKKILVRSALISLMSILPQSFADPVGSR----	TNDNKEGFYISAKYNPFSISHPRKFS	57
Db	1	MNYKKIFVSSALISLMSILPQSFADPVT	NDTGINDSREGFYISVKYNPFSISHPRKFS	60
Qy	58	EETPTNGNSLTKKVFGLLKGGDITTKDDFT	RVAPGIDFQNNLISGFSSIGYSMDGPRI	117
Db	61	EEAPINGNTSITKKVFGLLKGGDIAQSANF	NRTPDPALEFQNNLISGFSSIGYAMDGPRI	120
Qy	118	ELEAAYQOFNPKNTDNDNDTNGEYKHKFAL	RKDAEQYVVLKNDGITFMSLMVNTCY	177
Db	121	ELEAAYQKFDAKNPDNDNTSGDYKYKFGLS	REDALDKYVVLKNEGITFMSLMVNTCY	180
Qy	178	DITAEGVSFVPIYACAGIGADLITPDKNL	PKPAYQCKIGISYPTITPEVSAPIGGYHGV	237
Db	181	DITAEGVFPFIYACAGVGADLINVFKDFNL	KFSYQCKIGISYPTITPEVSAPIGGYHGV	240
Qy	238	GKNEKPIPVITPVLVNDAPQTTSASVTL	DVGFGGEGIGMRFTF	280
Db	241	GNNFNKIPVITPVLVLEGAPQTTSALVT	IDTGTGFGGEGVGRFTF	283
RESULT	9			
ID	ADA09737	standard; protein; 283 AA.		
XX	ADA09737;			
DT	06-NOV-2003	(first entry)		
XX	E. chaffeensis	outer membrane protein OMP-1B.		
DE				
XX	outer membrane protein; circulating	leukocyte; monocytic ehrlichiosis;		
KW	Rocky Mountain spotted fever;	canine ehrlichiosis; antigen.		
XX				
OS	Ehrlichia chaffeensis.			
XX	USG544517-B1.			
PN				
XX	08-APR-2003.			
PD				
XX	19-MAY-1999;	99US-00314701.		
PF				
XX	18-SEP-1998;	98US-0100843P.		
PR				
XX	(OHIS) UNIV OHIO STATE RES	FOUND.		
PA				
XX	Rikihisa Y, Ohashi N;			
PI				
XX	WPI: 2003-553952/52.			
DR	N-PSDB; ADA09736.			
XX				
PT	New isolated polynucleotide encoding	outer membrane protein P30 of		
PT	Ehrlichia canis or its variant or	fragment, useful for producing		
PT	Ehrlichia canis or Ehrlichia chaffeensis	outer membrane proteins for		
XX	diagnosing and treating ehrlichiosis.			
XX	Disclosure; Fig 4; 105pp; English.			
PS				
XX				
CC	The invention relates to an isolated	polynucleotide encoding a variant of		
CC	the outer membrane protein (OMP) P30	of Ehrlichia canis, an outer		
CC	membrane protein of E. canis, or an	antigenic fragment of the E. canis		
CC	P30 protein, or comprising a sequence	which is the complement of		
CC	nucleotide 99 through nucleotide 672	of ADA09764. Also disclosed are E.		
CC	canis and E. chaffeensis outer	membrane proteins and their encoding		
CC	nucleic acids. The polynucleotides	are useful for producing E. canis or		
CC	E. chaffeensis outer membrane	protein, for designing hybridisation probes		
CC	for isolating and identifying	cDNA and genomic clones encoding the OMP		
CC	or its allelic forms, for designing	primers for PCR. The polypeptides		
CC	encoded by the polynucleotide is	useful for diagnosing human ehrlichiosis		
CC	(Rocky mountain spotted fever) or	canine ehrlichiosis. The present		
CC	sequence represents an E. chaffeensis	outer membrane protein.		
XX				

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SQ      Sequence 283 AA;
Query Match      82.3%; Score 1202.5; DB 6; Length 283;
Best Local Similarity 79.5%; Pred. No. 3e-112;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

QY      1 MNYKKILVRSALISLMSILPYQSPADPVGSR---TNDNKEGFYISAKYNPSISHFRKPSA 57
DB      1 MNYKKIFVSSALISLMSILPYQSPADPVTSNDTGINDSREGFYISVKYNPSISHFRKPSA 60
QY      58 EETPINGTNSLTKKVFGKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYMDGPRI 117
DB      61 EEAPINGNTSITKKVFGKKGDDIAQSANFNRTDPALEFQNNLISGFGSGISGYAMDGPRI 120
QY      118 ELEAAVQQFNPKNTDNDNGEYKHFALSRKDAMEDQOYVVLKNDGITFMSLMVNTCY 177
DB      121 ELEAAVQKFDKPNPNNDNTSGDYKYFGLSREDAIADKKYVVLKNEGITFMSLMVNTCY 180
QY      178 DITAEGVSPVPYACAGIGADLITPKDLNLKFPAYQKGIGISYPIITPEVSAPFSGYHGV 237
DB      181 DITAEGVFPFIPYACAGVGADLINVFKDFNLKFSYQKGIGISYPIITPEVSAPFSGYHGV 240
QY      238 GNNFKKIPVITPVVLNDAPQTTASVTLDVGFGEIGMRFTF 280
DB      241 GNNFNKIPVITPVVLEGAPQTTASALVTIDTGYFGGEVGVRTF 283

RESULT 10
ADW04230
ID      ADW04230 standard; protein; 283 AA.
AC      ADW04230;
XX
XX
XX      24-MAR-2005 (first entry)
DE      Ehrlichia chaffeensis outer membrane protein (OMP), OMP-1B.
KW      DNA purification; diagnosis; outer membrane protein; OMP; P30F protein;
KW      infection; vaccine.
XX
OS      Ehrlichia chaffeensis.
FH      Key
FT      Peptide 1..25
FT      Protein /label= Signal_peptide
FT      Region /note= "Ehrlichia chaffeensis mature OMP protein"
FT      Region 26..41 /note= "Semivariable region (SV)"
FT      Region 82..94 /note= "Hypervariable region (HV1)"
FT      Region 145..163 /note= "Hypervariable region (HV2)"
FT      Region 248..272 /note= "Hypervariable region (HV3)"
XX
XX      US2004265334-A1.
XX
XX      30-DEC-2004.
XX
XX      29-JUL-2004; 2004US-00901774.
XX
XX      18-SEP-1998; 98US-0100843P.
XX      19-MAY-1999; 99US-00314701.
XX      28-JAN-2002; 2002US-00059964.
XX
XX      (RIKI/) RIKIHISA Y.
XX      (OHAS/) OHASHI N.
XX
XX      Rikihisa Y, Ohashi N;
XX      WPI; 2005-064871/07.
XX      N-PSDB; ADW04229.

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XX      New polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia
PT      canis or Ehrlichia chaffeensis, useful in preparing a composition for
PT      diagnosing or preventing E. canis or E. chaffeensis infection.
XX
PS      Disclosure; SEQ ID NO 4; 122pp; English.
XX
XX      The invention relates to nucleic acid sequences encoding outer membrane
CC      proteins (OMP) of Ehrlichia chaffeensis (designated as OMP proteins) and
CC      Ehrlichia canis (designated as P30F proteins). The OMP polynucleotide is
CC      useful in preparing a composition for diagnosing, treating or preventing
CC      an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present
CC      sequence is the Ehrlichia chaffeensis OMP protein.
XX
SQ      Sequence 283 AA;
Query Match      82.3%; Score 1202.5; DB 9; Length 283;
Best Local Similarity 79.5%; Pred. No. 3e-112;
Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

QY      1 MNYKKILVRSALISLMSILPYQSPADPVGSR---TNDNKEGFYISAKYNPSISHFRKPSA 57
DB      1 MNYKKIFVSSALISLMSILPYQSPADPVTSNDTGINDSREGFYISVKYNPSISHFRKPSA 60
QY      58 EETPINGTNSLTKKVFGKKGDDITKKDDFTRVAPGIDFQNNLISGFGSGISGYMDGPRI 117
DB      61 EEAPINGNTSITKKVFGKKGDDIAQSANFNRTDPALEFQNNLISGFGSGISGYAMDGPRI 120
QY      118 ELEAAVQQFNPKNTDNDNGEYKHFALSRKDAMEDQOYVVLKNDGITFMSLMVNTCY 177
DB      121 ELEAAVQKFDKPNPNNDNTSGDYKYFGLSREDAIADKKYVVLKNEGITFMSLMVNTCY 180
QY      178 DITAEGVSPVPYACAGIGADLITPKDLNLKFPAYQKGIGISYPIITPEVSAPFSGYHGV 237
DB      181 DITAEGVFPFIPYACAGVGADLINVFKDFNLKFSYQKGIGISYPIITPEVSAPFSGYHGV 240
QY      238 GNNFKKIPVITPVVLNDAPQTTASVTLDVGFGEIGMRFTF 280
DB      241 GNNFNKIPVITPVVLEGAPQTTASALVTIDTGYFGGEVGVRTF 283

RESULT 11
AAV06970
ID      AAV06970 standard; protein; 165 AA.
XX
XX      AAV06970;
AC
XX
XX      05-JUL-1999 (first entry)
DE      E. canis P30-10protein.
XX
XX      Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
KW      detection; dog.
XX
XX      Ehrlichia canis.
OS
XX
XX      WO9913720-A1.
XX
XX      25-MAR-1999.
XX
XX      18-SEP-1998; 98WO-US019600.
XX
XX      19-SEP-1997; 97US-0059353P.
XX
XX      (OHIS ) UNIV OHIO STATE.
XX
XX      Rikihisa Y, Ohashi N;
XX
XX      WPI; 1999-254290/21.
XX      N-PSDB; AAX34770.
XX
XX      Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia
PT      canis.

```

```
XX Disclosure; Fig 30B; 55pp; English.
XX
CC The invention provides isolated outer membrane proteins (OMP) from
CC Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
CC of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in
CC AAY06943-958. The E. canis proteins form part of the P30 family and
CC consist of proteins shown in AAY06959-970. The proteins and genes are
CC used to detect E. chaffeensis in patients and E. canis in dogs
XX
XX Sequence 165 AA;
Query Match 48.9%; Score 715; DB 2; Length 165;
Best Local Similarity 81.9%; Pred. No. 1.8e-63;
Matches 145; Conservative 4; Mismatches 16; Indels 12; Gaps 2;
QY 1 MNYKKILVRSALISLMSILPYQSPADPVGSRNDNKGFIYSAKYNPSISHFRKFSABET 60
DB 1 MNYKKILVRSALISLMSILPYQSPADPVGSRNDNKGFIYSAKYNPSISHFRKFSABET 60
QY 61 PINGTNSLTAKVFLGKKGDIKKODFTTRVAFGIDFQNNLISGFGSSIGYSMDGPRIELE 120
DB 61 PINGTNSLTAKVFLGKKGDIKKODFTTRVAFGIDFQNNLISGFGSSIGYSMDGPRIELE 120
QY 121 AAYQQNPNKNTDNDTNGEYKHFALSRKDAMEDDQQYVVLKNDGITFMSLMVNTCY 177
DB 121 AAYHNLIOKH-DNNDTDNGEYKHF-----YLVKMPWKISHMLFLKMTAY 165
RESULT 12
AAY06943
ID AAY06943 standard; protein; 281 AA.
AC AAY06943;
XX
DT 27-AUG-2003 (revised)
DT 05-JUL-1999 (first entry)
DE E. chaffeensis OMP-1 protein.
XX
KW Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
KW detection; dog.
XX
OS Ehrlichia chaffeensis.
XX
PN WO9913720-A1.
XX
PD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US019600.
XX
PR 19-SEP-1997; 97US-0059353P.
XX
PA (OHIS ) UNIV OHIO STATE.
XX
PI Rikihisa Y, Ohashi N;
XX
DR WPI; 1999-254290/21.
DR N-PSDB; AAX34743.
XX
PT Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia
PT canis.
XX
PS Disclosure; Fig 3B; 55pp; English.
XX
CC The invention provides isolated outer membrane proteins (OMP) from
CC Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
CC of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in
CC AAY06943-958. The E. canis proteins form part of the P30 family and
CC consist of proteins shown in AAY06959-970. The proteins and genes are
CC used to detect E. chaffeensis in patients and E. canis in dogs. (Updated
CC on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 281 AA;
Query Match 44.1%; Score 644.5; DB 2; Length 281;
Best Local Similarity 48.1%; Pred. No. 5e-56;
Matches 140; Conservative 41; Mismatches 89; Indels 21; Gaps 6;
QY 1 MNYKKILVRSALISLMSILPYQSPADPVGSRNDNKGFIYSAKYNPSISHFRKFSABET 60
DB 1 MNYKKVFTTSALISLISLPGVSFSDPAGSGINGN---FYISGKYMPASHFGEVFSABE- 56
QY 61 PINGTNSLTAKVFLGKKGDIKKODFTTRVAFGIDFQNNLISGFGSSIGYSMDG 114
DB 57 -----BRNTTVGVFLGKQNWGSAISNSPNDVFTVSNYSFKYENNPFLGFAAGIYSMDG 112
QY 115 PRIELEAAYQQNPNKNTDNDTNGEYKHFALSRKDAME----DQYVVLKNDGITFMS 170
DB 113 PRIELEVSVEYTFDVKNGNN--YKNEAHRYCALSHNSAADMSSASNNFVFLKNEGILLDIS 170
QY 171 LMVNTCYDITAGVSVFVPYACAGIGADLITIPKDLNLPAYQKGIGISYPIITPEVSAPFG 230
DB 171 FMLNACYDVVGEGIPFSPYICAGIGTDLVSMFEATNPKISYQGLGLSYISPEASVFIG 230
QY 231 GYHGVGNKEKIPVITPVVLDAPQ-TTSASVTLDVGYFGGEIGMRFTF 280
DB 231 GHFKHVIGNEFRDIPTIPTGTSLAGKGNYPVAILVDVCHFGIELGGRFVF 281
RESULT 13
AAU96105
ID AAU96105 standard; protein; 281 AA.
AC AAU96105;
XX
DT 07-AUG-2003 (revised)
DT 02-JUL-2002 (first entry)
DE Ehrlichia chaffeensis P28.
XX
KW Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
XX
OS Ehrlichia chaffeensis.
XX
PN WO200222782-A2.
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-US028759.
XX
PR 12-SEP-2000; 2000US-00660587.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Walker DH, Yu X, McBride JW;
XX
DR WPI; 2002-351882/38.
XX
PT New recombinant homologous 28 kilodalton immunodominant protein from
PT Ehrlichia canis, useful for treating Ehrlichia canis infections.
XX
PS Example 3; Fig 3; 106pp; English.
XX
CC The invention relates to a recombinant homologous 28 kDa immunodominant
CC protein, p28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably
CC dispersed in a pharmaceutically acceptable carrier, is useful for
CC inhibiting E. canis infection in a subject. (I) is useful in the
CC development of vaccines and serodiagnostics that are particularly
CC effective for disease prevention and serodiagnosis. AAU96100-AAU96118
CC represent the 28-kDa antigen amino acid sequences of the invention.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX
XX Sequence 281 AA;
Query Match 44.1%; Score 644.5; DB 5; Length 281;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:28:32 ; Search time 17.6732 Seconds
(without alignments)
646.394 Million cell updates/sec

Title: US-10-680-349-42_COPY_61_86
Perfect score: 136
Sequence: 1 PINGTNSLTKKVFLKKGDDITKDD 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	165	2	AAY06970 E. canis
2	136	100.0	280	5	Aau96116 Ehrlichia
3	136	100.0	280	5	Abg77958 Ehrlichia
4	136	100.0	280	6	Ada09781 E. canis
5	136	100.0	280	9	Adw04274 Ehrlichia
6	97	71.3	283	2	Aay06944 E. chaffee
7	97	71.3	283	5	Aau96106 Ehrlichia
8	97	71.3	283	5	Aau73413 Ehrlichia
9	97	71.3	283	5	Abg77936 Ehrlichia
10	97	71.3	283	6	Ada09737 E. chaffe
11	97	71.3	283	9	Adw04230 Ehrlichia
12	52.5	38.6	339	8	Adn21449 Bacterial
13	52	38.2	377	6	Abu29155 Protein e
14	52	38.2	378	7	Adh88024 Enterococ
15	52	38.2	481	6	Abu20708 Protein e
16	51	37.5	525	8	Adsa4601 Bacterial
17	50.5	37.1	873	8	Adsa2299 Bacterial
18	50	36.8	283	9	Adw04295 Cowdria r
19	50	36.8	284	5	Aau96111 Cowdria r
20	50	36.8	302	6	Abp79144 N. gonorr
21	50	36.8	302	6	Abp76775 N. gonorr
22	49.5	36.4	521	7	Abc23592 Rickettsi
23	49	36.0	235	9	Adw17535 Pinus rad
24	49	36.0	345	7	Adc00818 Enterohae

25	49	36.0	472	8	Adn46936 Thermococ
26	49	36.0	511	5	Abp65734 Bifidobac
27	49	36.0	577	5	Abp27646 Streptoco
28	49	36.0	577	6	Abu46702 Protein e
29	49	36.0	629	7	Adg68790 Streptoco
30	49	36.0	629	8	Adj61994 Group A s
31	49	36.0	1992	2	Aaw04505 Moraxella
32	49	36.0	1992	4	Aab69137 M. catarr
33	49	36.0	1992	4	Aab69133 M. catarr
34	49	36.0	2047	4	Aab69134 M. catarr
35	48.5	35.7	416	2	Aar74151 Mango cia
36	48.5	35.7	416	2	Aaw44331 Class II
37	48.5	35.7	476	4	Abg99093 Pyrococcu
38	48.5	35.7	476	8	Adl23827 Pyrococcu
39	48.5	35.7	557	4	Aau20133 Human DNA
40	48.5	35.7	557	5	Abg91382 Novel hum
41	48.5	35.7	585	8	Adg32050 Mutant B
42	48.5	35.7	594	8	Adg32068 Mutant B
43	48.5	35.7	616	6	Abra41881 Predicted
44	48.5	35.7	616	6	Aae36781 Human cas
45	48.5	35.7	645	2	Aaw29653 Human sec

ALIGNMENTS

RESULT 1
AAY06970
ID AAY06970 standard; protein; 165 AA.
XX
AC AAY06970;

DT 05-JUL-1999 (first entry)
XX
DE E. canis P30-10protein.
XX
KW Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
KW detection; dog.
XX
OS Ehrlichia canis.
XX
PN WO9913720-A1.
XX
PD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US019600.
XX
PR 19-SEP-1997; 97US-0059353P.
XX

XX (OHIS) UNIV OHIO STATE.
XX Rikihisa V, Ohashi N;
XX
DR WPI; 1999-254290/21.
XX N-PSDB; AAX34770.
XX Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis.
XX
PS Disclosure; Fig 30B; 55pp; English.
XX

XX The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in CC AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs
XX Sequence 165 AA;
SQ

Query Match 100.0%; Score 136; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 PINGTNSLTKKVFGGLKKGDTTKDD 26
DB      61 PINGTNSLTKKVFGGLKKGDTTKDD 86

RESULT 2
AAU96116
ID      AAU96116 standard; protein; 280 AA.
XX
AC      AAU96116;
XX
DT      02-JUL-2002 (first entry)
XX
DE      Ehrlichia canis p28-2.
XX
KW      Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
XX
OS      Ehrlichia canis.
XX
PN      WO20022782-A2.
XX
XX      21-MAR-2002.
XX
PF      12-SEP-2001; 2001WO-US028759.
XX
PR      12-SEP-2000; 2000US-00660587.
XX
PA      (RERE-) RES DEV FOUND.
XX
PI      Walker DH, Yu X, McBride JW;
XX
XX      WPI; 2002-351882/38.
DR      N-PSDB; ABK68876.
XX
XX      New recombinant homologous 28 kilodalton immunodominant protein from
PT      Ehrlichia canis, useful for treating Ehrlichia canis infections.
XX
XX      Claim 16; Fig 14; 106pp; English.
XX
CC      The invention relates to a recombinant homologous 28 kDa immunodominant
CC      protein, P28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably
CC      dispersed in a pharmaceutically acceptable carrier, is useful for
CC      inhibiting E. canis infection in a subject. (I) is useful in the
CC      development of vaccines and serodiagnostics that are particularly
CC      effective for disease prevention and serodiagnosis. AAU96100-AAU96118
CC      represent the 28-kDa antigen amino acid sequences of the invention
XX
XX      Sequence 280 AA;

Query Match      100.0%; Score 136; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PINGTNSLTKKVFGGLKKGDTTKDD 26
DB      61 PINGTNSLTKKVFGGLKKGDTTKDD 86

RESULT 3
ABG77958
ID      ABG77958 standard; protein; 280 AA.
XX
AC      ABG77958;
XX
DT      15-NOV-2002 (first entry)
XX
DE      Ehrlichia canis outer membrane protein (P30F) #9.
XX
KW      Outer membrane protein; OMP; P30F; ehrlichiosis; infection.
XX
OS      Ehrlichia canis.
XX

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PN      US2002120115-A1.
XX
PD      29-AUG-2002.
XX
PF      28-JAN-2002; 2002US-00059964.
XX
PR      19-MAY-1999; 99US-00314701.
XX
XX      (RIKI/) RIKIHISA Y.
PA      (OHAS/) OHASHI N.
XX
PI      Rikihisa Y, Ohashi N;
XX
DR      WPI; 2002-618954/66.
DR      N-PSDB; ABS63299.
XX
PT      Isolated polynucleotide encoding an outer membrane protein of E. canis or
PT      E. chaffeensis used in the diagnosis of infection.
XX
PS      Claim 10; Fig 30B; 49pp; English.
XX
CC      The invention relates to an isolated polynucleotide encoding an outer
CC      membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used
CC      in the diagnosis of infection. An infection such as human ehrlichiosis or
CC      canine ehrlichiosis can be diagnosed by providing a serum sample from the
CC      patient, providing a polypeptide or mixture of polypeptides, contacting
CC      the sample with the polypeptide and assaying for the formation of a
CC      complex between antibodies in the serum sample and the polypeptide, where
CC      formation of a complex is indicative of infection with E. chaffeensis.
CC      This sequence represents an Ehrlichia outer membrane protein of the
CC      invention
XX
XX      Sequence 280 AA;

Query Match      100.0%; Score 136; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PINGTNSLTKKVFGGLKKGDTTKDD 26
DB      61 PINGTNSLTKKVFGGLKKGDTTKDD 86

RESULT 4
ADA09781
ID      ADA09781 standard; protein; 280 AA.
XX
AC      ADA09781;
XX
XX      06-NOV-2003 (first entry)
DT
DE      E. canis outer membrane protein P30-10.
XX
KW      outer membrane protein; circulating leukocyte; monocytic ehrlichiosis;
KW      Rocky Mountain spotted fever; canine ehrlichiosis; antigen.
XX
OS      Ehrlichia canis.
XX
PN      US6544517-B1.
XX
PD      08-APR-2003.
XX
PF      19-MAY-1999; 99US-00314701.
XX
PR      18-SEP-1998; 98US-0100843P.
XX
XX      (OHIS ) UNIV OHIO STATE RES FOUND.
PA
PI      Rikihisa Y, Ohashi N;
XX
DR      WPI; 2003-553952/52.
DR      N-PSDB; ADA09780.
XX

```


PT New isolated polynucleotide encoding outer membrane protein P30 of
PT Ehrlichia canis or its variant or fragment, useful for producing
PT Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins for
PT diagnosing and treating ehrlichiosis.
XX
PS Disclosure; Fig 30; 105pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a variant of
CC the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer
CC membrane protein of E. canis, or an antigenic fragment of the E. canis
CC P30 protein, or comprising a sequence which is the complement of
CC nucleotide 99 through nucleotide 672 of ADA09764. Also disclosed are E.
CC canis and E. chaffeensis outer membrane proteins and their encoding
CC nucleic acids. The polynucleotides are useful for producing E. canis or
CC E. chaffeensis outer membrane protein, for designing hybridisation probes
CC for isolating and identifying cDNA and genomic clones encoding the OMP
CC or its allelic forms, for designing primers for PCR. The polypeptides
CC encoded by the polynucleotide is useful for diagnosing human ehrlichiosis
CC (Rocky mountain spotted fever) or canine ehrlichiosis. The present
CC sequence represents an E. canis outer membrane protein.
XX
SQ Sequence 280 AA;
Query Match 100.0%; Score 136; DB 6; Length 280;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PINGTNSLTGKVFGLKKGDIKKDD 26
DB 61 PINGTNSLTGKVFGLKKGDIKKDD 86
RESULT 5
ADW04274
ID ADW04274 standard; protein; 280 AA.
XX
AC ADW04274;
XX
DT 24-MAR-2005 (first entry)
DE Ehrlichia canis outer membrane protein (P30F), P30-10.
XX
KW DNA purification; diagnosis; outer membrane protein; OMP; P30F protein;
KW infection; vaccine.
XX
OS Ehrlichia canis.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= Signal_peptide
FT Protein 26..280
FT /note= "Ehrlichia canis mature OMP protein"
XX
PN US2004265334-A1.
XX
PD 30-DEC-2004.
XX
PF 29-JUL-2004; 2004US-00901774.
XX
PR 18-SEP-1998; 98US-0100843P.
PR 19-MAY-1999; 99US-00314701.
PR 28-JAN-2002; 2002US-00059964.
XX
PA (RIKI/) RIKIHISA Y.
PA (OHAS/) OHASHI N.
XX
PI Rikihisa Y, Ohashi N;
XX
DR WPI; 2005-064871/07.
DR N-PSDB; ADW04273.
XX
XX New polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia
PT canis or Ehrlichia chaffeensis, useful in preparing a composition for

PT diagnosing or preventing E. canis or E. chaffeensis infection.
XX
PS Claim 10; SEQ ID NO 48; 122pp; English.
XX
CC The invention relates to nucleic acid sequences encoding outer membrane
CC proteins (OMP) of Ehrlichia chaffeensis (designated as OMP proteins) and
CC Ehrlichia canis (designated as P30F proteins). The OMP polynucleotide is
CC useful in preparing a composition for diagnosing, treating or preventing
CC an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present
CC sequence is the Ehrlichia canis P30F protein.
XX
SQ Sequence 280 AA;
Query Match 100.0%; Score 136; DB 9; Length 280;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PINGTNSLTGKVFGLKKGDIKKDD 26
DB 61 PINGTNSLTGKVFGLKKGDIKKDD 86
RESULT 6
AY06944
ID AY06944 standard; protein; 283 AA.
XX
AC AY06944;
XX
DT 27-AUG-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
DE E. chaffeensis OMP-1B protein.
XX
KW Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
KW detection; dog.
XX
OS Ehrlichia chaffeensis.
XX
PN WO9913720-A1.
XX
PD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US019600.
XX
PR 19-SEP-1997; 97US-0059353P.
XX
PA (OHIS) UNIV OHIO STATE.
XX
PI Rikihisa Y, Ohashi N;
XX
DR WPI; 1999-254290/21.
DR N-PSDB; AAX34744.
XX
PT Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia
PT canis.
XX
PS Claim 12; Fig 4B; 55pp; English.
XX
CC The invention provides isolated outer membrane proteins (OMP) from
CC Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
CC of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in
CC AAY06943-958. The E. canis proteins form part of the P30 family and
CC consist of proteins shown in AAY06959-970. The proteins and genes are
CC used to detect E. chaffeensis in patients and E. canis in dogs. (Updated
CC on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 283 AA;
Query Match 71.3%; Score 97; DB 2; Length 283;
Best Local Similarity 78.3%; Pred. No. 4.2e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 PINGTNSLTGKVFGLKKGDIKKDD 23

```

Db      ||||| |:|||||:|||||:
        64 PINGNTSITKKVFGKKGDDIAQ 86

RESULT 7
AAU96106
ID AAU96106 standard; protein; 283 AA.
XX
AC AAU96106;
XX
DT 07-AUG-2003 (revised)
DT 02-JUL-2002 (first entry)
XX
DE Ehrlichia chaffeensis OMP-1B.
XX
KW Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
XX
OS Ehrlichia chaffeensis.
XX
PN WO200222782-A2.
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-US028759.
XX
PR 12-SEP-2000; 2000US-00660587.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Walker DH, Yu X, McBride JW;
XX
DR WPI; 2002-351882/38.
XX
PT New recombinant homologous 28 kilodalton immunodominant protein from
PT Ehrlichia canis, useful for treating Ehrlichia canis infections.
XX
PS Example 3; Fig 3; 106pp; English.
XX
CC The invention relates to a recombinant homologous 28 kDa immunodominant
CC protein, P28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably
CC dispersed in a pharmaceutically acceptable carrier, is useful for
CC inhibiting E. canis infection in a subject. (I) is useful in the
CC development of vaccines and serodiagnostics that are particularly
CC effective for disease prevention and serodiagnosis. AAU96100-AAU96118
CC represent the 28-kDa antigen amino acid sequences of the invention.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX
XX Sequence 283 AA;

Query Match 71.3%; Score 97; DB 5; Length 283;
Best Local Similarity 78.3%; Pred. No. 4.2e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGNTSLTKKVFGLKKGDDITK 23
Db      ||||| |:|||||:|||||:
        64 PINGNTSITKKVFGKKGDDIAQ 86

RESULT 8
AAU73413
ID AAU73413 standard; protein; 283 AA.
XX
AC AAU73413;
XX
DT 12-MAR-2002 (first entry)
XX
DE Ehrlichia chaffeensis outer membrane protein P28-14.
XX
KW Ehrlichia; outer membrane protein; P28; antibiotic; vaccine.
XX
OS Ehrlichia chaffeensis.
XX
PN WO200183699-A2.

Query Match 71.3%; Score 97; DB 5; Length 283;
Best Local Similarity 78.3%; Pred. No. 4.2e-06;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGNTSLTKKVFGLKKGDDITK 23
Db      ||||| |:|||||:|||||:
        64 PINGNTSITKKVFGKKGDDIAQ 86

RESULT 9
ABG77936
ID ABG77936 standard; protein; 283 AA.
XX
AC ABG77936;
XX
DT 15-NOV-2002 (first entry)
XX
DE Ehrlichia chaffeensis outer membrane protein (OMP) #2.
XX
KW Outer membrane protein; OMP; P30F; ehrlichiosis; infection.
XX
OS Ehrlichia chaffeensis.
XX
PN US2002120115-A1.
XX
PD 29-AUG-2002.
XX
PF 28-JAN-2002; 2002US-00059964.
XX
PR 19-MAY-1999; 99US-00314701.
XX
PA (RIKI/) RIKIHISA Y.
PA (OHAS/) OHASHI N.
XX
PI Rikihisa Y, Ohashi N;
XX
DR WPI; 2002-618954/66.
DR N-PSDB; ABS63277.
XX
PT Isolated polynucleotide encoding an outer membrane protein of E. canis or
PT E. chaffeensis used in the diagnosis of infection.
XX
PS Disclosure; Fig 4B; 49pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding an outer
CC membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used

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CC in the diagnosis of infection. An infection such as human ehrlichiosis or
 CC canine ehrlichiosis can be diagnosed by providing a serum sample from the
 CC patient, providing a polypeptide or mixture of polypeptides, contacting
 CC the sample with the polypeptide and assaying for the formation of a
 CC complex between antibodies in the serum sample and the polypeptide, where
 CC formation of a complex is indicative of infection with *E. chaffeensis*.
 CC This sequence represents an Ehrlichia outer membrane protein of the
 CC invention
 XX
 XX Sequence 283 AA;

Query Match 71.3%; Score 97; DB 5; Length 283;
 Best Local Similarity 78.3%; Pred. No. 4.2e-06;
 Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKKGDDITK 23
 ||||| :||||| :
 Db 64 PINGNTSITKKVFGKKGDDIAQ 86

RESULT 10
 ADA09737
 ID ADA09737 standard; protein; 283 AA.

XX AC ADA09737;
 XX DT 06-NOV-2003 (first entry)
 XX DE *E. chaffeensis* outer membrane protein OMP-1B.

XX outer membrane protein; circulating leukocyte; monocytic ehrlichiosis;
 KW Rocky Mountain spotted fever; canine ehrlichiosis; antigen.

XX Ehrlichia chaffeensis.

XX US6544517-B1.

XX 08-APR-2003.

XX 19-MAY-1999; 99US-00314701.

XX 18-SEP-1998; 98US-0100843P.

XX (OHIS) UNIV OHIO STATE RES FOUND.

XX Rikihisa Y, Ohashi N;

XX WPI; 2003-553952/52.

XX N-PSDB; ADA09736.

XX New isolated polynucleotide encoding outer membrane protein P30 of
 PT Ehrlichia canis or its variant or fragment, useful for producing
 PT Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins for
 PT diagnosing and treating ehrlichiosis.

XX Disclosure; Fig 4; 105pp; English.

XX The invention relates to an isolated polynucleotide encoding a variant of
 CC the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer
 CC membrane protein of *E. canis* , or an antigenic fragment of the *E. canis*
 CC P30 protein, or comprising a sequence which is the complement of
 CC nucleotide 99 through nucleotide 672 of ADA09764. Also disclosed are *E.*
 CC canis and *E. chaffeensis* outer membrane proteins and their encoding
 CC nucleic acids. The polynucleotides are useful for producing *E. canis* or
 CC *E. chaffeensis* outer membrane protein, for designing hybridisation probes
 CC for isolating and identifying cDNA and genomic clones encoding the OMP
 CC or its allelic forms, for designing primers for PCR. The polypeptides
 CC encoded by the polynucleotide is useful for diagnosing human ehrlichiosis
 CC (Rocky mountain spotted fever) or canine ehrlichiosis. The present
 CC sequence represents an *E. chaffeensis* outer membrane protein.

XX Sequence 283 AA;

Query Match 71.3%; Score 97; DB 9; Length 283;
 Best Local Similarity 78.3%; Pred. No. 4.2e-06;

Query Match 71.3%; Score 97; DB 6; Length 283;
 Best Local Similarity 78.3%; Pred. No. 4.2e-06;
 Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKKGDDITK 23
 ||||| :||||| :
 Db 64 PINGNTSITKKVFGKKGDDIAQ 86

RESULT 11
 ADW04230
 ID ADW04230 standard; protein; 283 AA.

XX AC ADW04230;

XX DT 24-MAR-2005 (first entry)

XX DE Ehrlichia chaffeensis outer membrane protein (OMP), OMP-1B.

XX DNA purification; diagnosis; outer membrane protein; OMP; P30F protein;
 KW infection; vaccine.

XX OS Ehrlichia chaffeensis.

XX FH Key Location/Qualifiers

FT Peptide 1..25
 FT Protein /label= Signal_peptide

FT Region /note= "Ehrlichia chaffeensis mature OMP protein"

FT Region /note= "Semivariable region (SV)"

FT Region /note= "Hypervariable region (HV1)"

FT Region /note= "Hypervariable region (HV2)"

FT Region /note= "Hypervariable region (HV3)"

XX US2004265334-A1.

XX 30-DEC-2004.

XX 29-JUL-2004; 2004US-00901774.

XX 18-SEP-1998; 98US-0100843P.

XX 19-MAY-1999; 99US-00314701.

XX 28-JAN-2002; 2002US-00059964.

XX (RIKI/) RIKIHISA Y.

XX (OHAS/) OHASHI N.

XX Rikihisa Y, Ohashi N;

XX WPI; 2005-064871/07.

XX N-PSDB; ADW04229.

XX New polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia
 PT canis or Ehrlichia chaffeensis, useful in preparing a composition for
 PT diagnosing or preventing *E. canis* or *E. chaffeensis* infection.

XX Disclosure; SEQ ID NO 4; 122pp; English.

XX The invention relates to nucleic acid sequences encoding outer membrane
 CC proteins (OMP) of Ehrlichia chaffeensis (designated as OMP proteins) and
 CC Ehrlichia canis (designated as P30F proteins). The OMP polynucleotide is
 CC useful in preparing a composition for diagnosing, treating or preventing
 CC an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present
 CC sequence is the Ehrlichia chaffeensis OMP protein.

XX Sequence 283 AA;

Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGGLKKGDDITK 23
DB 64 PINGNTSITKKVFGGLKKGDDIAQ 86

RESULT 12
ADN21449
ID ADN21449 standard; protein; 339 AA.
AC ADN21449;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #4102.
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 4102; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 339 AA;
Query Match 38.6%; Score 52.5; DB 8; Length 339;
Best Local Similarity 44.4%; Pred. No. 31;
Matches 12; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 PINGTNSLTKKVF-GLKKGDDITKKDD 26
DB 198 PLNGSESVWKKVLQGLEKEGEGTRDKD 224

RESULT 13
ABU29155
ID ABU29155 standard; protein; 377 AA.
XX
AC ABU29155;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #14682.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Enterococcus faecalis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlseen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA33025.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 57079; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent

CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 481 AA;

Query Match 38.2%; Score 52; DB 6; Length 481;

Best Local Similarity 42.3%; Pred. No. 57;

Matches 11; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 PINGTNSLTQKVFGLKKGGDITKDD 26

Db 147 PFGGNDLKEKIIRTPLDPDITFSD 172

Search completed: January 24, 2006, 11:42:47
 Job time : 19.6732 secs